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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-09-68-740A-1
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US-09-908-322-12
US-09-908-322-13
US-08-872-855-2
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                         APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPRAX: 212-869-8864
ITELERAX: 6141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: «UNROWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: "Unknown;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-908-322-2
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 728 amino acida
TYPE: amino acid
STRANDEDNESS: <Unknown>
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                                                                                           SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
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US-09-908-322-2
; Sequence 2, Application US/09908322
; Patent No. 6783956
; Patent INFORMATION:
; GENERAL INFORMATION:
; Henrique, Domingos Manuel Pinto
: Lewis, Julian Hart
: Lewis, Julian Hart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gray, Grace
Gray, Grace
INVENTION: NUCLECTIDE AND PROTEIN
VERTEBRATE DELTA GENE P
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ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF SEQUENCES:
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241 HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300
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APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domisgos Manuel Pinto
APPLICANT: Herrique, Domisgos Manuel Pinto
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                          CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                                                                                                                                                                                                                                                                                                                 CANGAQ-CVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDXSCTCPPG
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                                                                                                                                              301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
                                                                                                                                                                       HHKPCKNGATCTNTGOGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
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SOFTWARE: FEBASEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ARLIer, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-981-392-5
Sequence 5, Application US/08981392
Patent No. 6262025
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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DECIIATEV 729
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                                                                                                  KEEHGKCEAKCETYDSEAEEKSAVQLKSSDTSERKRPDSVXSTSKDTKYQSVYVISEEKD
                   LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/072,855 ~> 08/6 32,637 FILING DATE: 11-JUN-1997 CLASSIPICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Arnold, Beth 8: Arnold, Beth 8: Arnold, Beth 8: REFERENCE/DOCKET NUMBER: 35,430 REFERENCE/DOCKET NUMBER: MAA-003.02 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION: 017-032-1000
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                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08872855

Patent No. 6121045

GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
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Best Local Similarity 99.9
Matches 728; Conservative
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: unknown
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Best Local Similarity 82.2
Matches 600; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-908-322-5
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                                                                                                                                                                                                                                                                                                                                                                                                         115 GFTWPCTFSLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELK 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCPPGFYGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCEKKIDYCSSN 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPG 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 PCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCPPG 474
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                                                                                                                                                                                                      DB 3;
                                                                                                                                                                                                    84.2%; Score 3495.5; DB 3
82.2%; Pred. No. 3.7e-255;
ive 65; Mismatches 54;
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US-09-908-322-5
; Sequence 5, Application US/09908322
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                    Best Local Similarity 82.2
Matches 600; Conservative
                                                                                                                                                 MOLECULE TYPE: peptide
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GENERAL INFORMATION:
Henrique, Domingos Manuel Pinto
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Grace DB 4; 84.2%; Score 3495.5; DB 4 82.2%; Pred. No. 3.7e-255; COMPUTER: 1036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARRE: FRASISCO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-7u1-2001
CLASSIFICATION: <unhoranteer companies of the c CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York 65; Mismatches 300 셤

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US-09-23-753-27

Sequence 27, Application US/09423753

Patent No. 6664098

GENERAL INFORMATION:
PILE REPRENCE: KP-863;
FILE REPRENCE: KP-863;
CURRENT APPLICATION NUMBER: US/09/423,753

CURRENT FILING DATE: 1999-12-30

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-14

PRIOR FILING DATE: 1998-05-14

PRIOR FILING DATE: 1998-05-14

NUMBER OF SEQ ID NOS: 27

SOFUMARE: PATCHING VALENCE: 1997-05-14

SOFUMARE: PATCHING VALENCE: 1997-05-14
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84.1%; Score 3494.5; DB 4

Best Local Similarity 83.3%; Pred. No. 4.4e-255;

Matches 609; Conservative 47; Mismatches 64;
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EKDECVIATEV 723
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ORGANISM: Homo sapiens
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APPLICANT: INFORMATION:

APPLICANT: ITOH, AKIRA

TITLE OF INVENTION: BIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE

FILE REFERENCE: KP-8447

CURRENT APPLICATION NUMBER: US/09/068,740A

CURRENT FILING DATE: 1998-06-18

PRIOR APPLICATION NUMBER: JP 7-299611

PRIOR PELING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-16

PRIOR FILING DATE: 1996-11-15

PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PARENTIN VET. 2.1

SEQ ID NOS: 48
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83.3%; Pred. No. 4.4e-255;
ive 47; Mismatches 64; Indels 11;
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ORGANISM: Homo sapiens
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Best Local Similarity 83.3%
Matches 609; Conservative
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Prior Application removed
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
LENGTH: 723
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EKDECVIATEV
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                                      TYPE: PRT
CRGANISM: Homo
US-10-140-002-346
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                     FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATORHLTVGEEWSQDLHSGRTDLKY
                                                          174 SYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ
                                                                                                HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
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          FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY
                                               SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 346, Application US/10140002
Patent No. 6725730
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Flyazoff, Bllen
Gao, Wei-Glang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Wood, William
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EKDECVIATEV 723
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US-10-140-002-346
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DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
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                                             Gaps
                                             11;
  723;
  Length
84.1%; Score 3494.5; DB 4; Length
83.3%; Pred. No. 4.4e-255;
ive 47; Mismatches 64; Indels
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US-08-872-855-7
; Sequence 7. Application US/08872855
; Patent No. 61.21045
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean
; APPLICANT: McCarthy, David
; APPLICANT: McCarthy, Sean
; TITLE OF INVENTION: NOVEL HUMAN DELIA3 COMPOSITIONS AND
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420 413 480 473

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CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY 480
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                                   TEKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHOPEACRSETETMN
                                                   61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Vivien Chan et al.
TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND UTILE OF INVENTION: NOTCH RECEPTOR LIGANDS AND UTILE REFERENCE: PPO-1602.002 / 200130.498
CURRENT APPLICATION NUMBER: US/09/641,612
CURRENT FILING DATE: 2000-08-17
NUMBER OF SEG ID NOS: 10
SOFTWARE: FASICEO for Windows Version 4.0
SOFTUNO 6.
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; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-09-641-612-6
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TITLE OF INVENTION: THERAPEUTIC USES THEREFOR NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
CONFUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-UNN-1997
CLASSIFICATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
TELECAMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TTPES: amino acids
TTPES: TENGTH: SINGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

84.1%; Score 3491.5; DB 3;
Best Local Similarity 82.1%; Pred. No. 7.4e-255;
Matches 599; Conservative 65; Mismatches 55;
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MOLECULE TYPE: protein
US-08-872-855-7
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444 GRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATC 503
                       356 NGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQAGFS 415
                                                                                                                                                                                      623
                                                                                                                                                                                                                                                                        624 NKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-SVKEEHGKCEAKCETYDSEAEEK 681
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                                                                                                                                                                   HERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEKYTEGQNSQFPWIAVCAGIILV
                                                                                                                                                                                                                                                   LMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKDISISVIGATQIKNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.3%; Score 3375; DB 3;
79.2%; Pred. No. 4.4e-246;
iive 71; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOS:
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
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NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFRENCE/DOCKET NUMBER: MAA.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acids
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amino acid
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Matches 579; Conservative
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TOPOLOGY: 1:
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                                                                                                                                                                     84 TYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLT 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 DAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGRYCDE 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 RPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNCELSAMTCADGPCF 383
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1 SGVFELKLOEFVNKKGLLGNRNCCR----GGAGPPPCACRTFFRVCLKHYQASVSPEPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 DRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGRYCDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | APPLICANT: SAKANO, SELJI |
| APPLICANT: SAKANO, SELJI |
| APPLICANT: ITOH, AKIRA |
| TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE |
| TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE |
| TITLE OF INVENTION: NUMBER: US/09/068,740A |
| CURRENT FILING DATE: 1998-06-18 |
| PRIOR APPLICATION NUMBER: UP 7-299611 |
| PRIOR FILING DATE: 1995-11-17 |
| PRIOR FILING DATE: 1995-11-17 |
| PRIOR FILING DATE: 1995-11-16 |
| PRIOR PILING DATE: 1996-11-15 |
| NUMBER OF SEQ ID NOS: 48 |
| SOFTWARE: PATENTIN VOY: 2.1 |
| SEQ ID NO 4 |
| LENGTH: 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09068740A Patent No. 6337387 GENERAL INFORMATION:
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Best Local Similarity 84.0 Matches 595; Conservative
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ORGANISM: Homo sapiens
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US-09-068-740A-4
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOSS
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION WUBBE: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEG 1D NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.51
Matches 574; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application Us/08981392
Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: ISA-HOTOWICz, David
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Taskonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
                                                          290 THHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSPSC
                           MGRRSALALAVVSALL -- CQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGP----P
                                                                                                                                      GPTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLK
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STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
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EKDECVIATEV 720
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-08-981-392-12
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THHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSC 359
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                                      172 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDD
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APPLICANT: MCCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Tab PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REFERENCES/DOCKET NUMBER: 35,430
REFERENCES/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-872-855-5; Sequence 5, Application US/08872855; Patent No. 6121045
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STATE: MA
COUNTRY: USA
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60 CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF 119
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78.5%; Pred. No. 1.5e-245;
tive 73; Mismatches 72;
                                                                                                                                                                                                                                      APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
FILING DATE: 17-U1-2001
CLASSIFICATION NUMBER: US/09/908,322
FILING DATE: 17-U1-2001
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 212-790-9990
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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LENGTH: 722 amino acide
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                  Sequence 12, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
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Best Local Similarity 78.5°
Matches 574; Conservative
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712 EKDECVIATEV 722
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US-09-908-322-12
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                                                                                                                                                                                                                                                                                                            Query Match
80.6%; Score 3346.5; DB 3; Length 713;
Best Local Similarity 78.5%; Pred. No. 6.2e-244;
Matches 574; Conservative 67; Mismatches 69; Indels 21;
TELEPHONE: 617-832-1000
TELEPAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino 
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EKDECVIATEV 713
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Search completed: November 29, 2004, 13:28:01 Job time : 23.3912 secs This Page Blank (uspto)

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WO9701571-A1
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Aaw1719 C-Delta-1
Aaw179029 Chick del
Aaw18353 Prolifera
Aaw94498 Human del
Aaw94498 Human del
Aaw94298 Human DRO
Aab53422 Human PRO
Aab53422 Human PRO
Aab1244 Human PRO
Aab12348 Human PRO
Aab1234 Human PRO
Abb35064 Human RO
Abu85023 Novel Bec
Abu6742 Human PRO
Abu89823 Novel Bec
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1 MGGRFLLTLALLSALLCRCQ......YQSVYVISEEKDECIIATEV 728
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                           2002273 segs, 358729299 residues
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Listing first 45 summaries
                                   - protein search, using sw model
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C-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma; neurogenesis; therapy.
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ADB15938
ADA4724
ADA67519
ADB30526
ADA86822
ADA91334
ADA9171
ADB14814
ADB14814
ADB14814
ADB19906
ADB19906
ADB19906
ADB193218
ADA74472
ADA74105
ADB2229
ADA75192
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/label= EGF1
262. 293. 332
293. 332
333. 370
/label= EGF4
371. 409
/label= EGF5
410. 447
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'note= "transmembrane domain"

96WO-US011178. 95US-0000589P. N

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New vertebrate Delta protein, DNA and antibodies - for treating and
preventing cancer, nervous system disorders and for tissue regeneration.
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                  LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSV
                                                           KEEHGKCEAKCETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISBEKD
LANCOREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSV
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label= EGF7
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/label= EGF8
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/label= EGF2
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/label= EGF3
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/label= EGF1
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/label= EG
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                                                                                                                                                                                                                               C-delta-1 polypeptide (AAW00876) is the chick homologue of Drosophila Delta, a protein that binds to Notch protein. Expression of C-Delta-1 correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (AATS8888) obtd. from chick stage 4-6 terminal amino acids of the longer version, was also isolated, and mouse (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders or colon cancer, melanoma or seminoma, and nervous system disorders promote tissue regeneration and repair
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iive 0; Mismatches 0;
                                                              Lewis J,
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DCKTPFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LANCQREKDISISVIGATQIKUTUKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSV 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEEHGKCEAKCETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKD 719
                                              C-delta-1 polypeptide (AAW11719) is the chick homologue of Drosophila Delta, a protein that binds to Notch protein. Expression of C-Delta-1 correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (AAT58897) obtd. from chick stage 4-6 embryos. An alternatively spliced variant (AAW00876) was also isolated, and mouse (AAW1720) and human (AAW1721-38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                          99.2%; Score 4119.5; DB 2; Length 727; 99.6%; Pred. No. 5.7e-226; ive 0; Mismatches 2; Indels 1;
                                                                                                                                                                                                                                                                                                                 disorders or to promote tissue regeneration and repair
Disclosure, Fig 2; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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ECIIATEV
                                                                                                                                                                                                                                                                                                                                                                     Seguence 727 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725;
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This sequence represents the chick delta protein amino acid sequence.

Delta is a toporythmic protein that contains a sequence which is cleaved

CC by the metalloprotease-disining kuzbanian (Kuz). Cleavage by Kuz

results in two fragments, a soluble amino terminal fragment consisting

cessentially of the extracellular domain, and a membrane bound fragment

CC consisting of the transmembrane domain and the intracellular domain. The

soluble fragment is able to bind to Notch. Delta plays a key role in

differentiation, and therefore detection and measurement of delta

activation is important in the study of differentiation. The invention

cativation is important in the study of differentiation. The invention

contained for detecting and measuring delta activation. Delta cleavage

competides, and chimeric proteins are useful for modulating the activity of

Notch, delta or kuz or at least one of the signalling pathways in a cell

con organism, expressing Notch. By contacting a cell with kuz protein is

modulated and vice versa. A delta cleavage peptide or its derivative

conclusion such as cervical, breast, colon or lung cancer, melanoma or

capable of binding kuz protein is useful for treating or preventing a

clisease or disorder associated with increased delta activity or

capable of summans. A recombinant cell comprising a delta peptide is

capable of disorder associated with increased delta activity or

capable of summans. A recombinant cell comprising a delta peptide is

capable of disorder associated with increased delta activity or

capable of disorder associated with increased delta activity or

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capable of delta cleavage peptide is useful for the disgnosis of diseases or

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capable or diso
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cleavage peptide, nucleic acids and antibodies useful for diagnosis, prevention and treatment of cancer, disorders of central nervous system,
                                                                                                                                                                                                                                                                       lung, melanoma; seminoma; central nervous system disorder; psoriasis; tissue regeneration; liver cirrhosis; keloid formation; baldness; inner ear disorder; chick.
                                                                                                                                                                                                                                                  colon; cancer;
                                                                                                                                                                                                                                                  differentiation; cervical; breast;
                                                                                                                                                                                                 Chick delta protein amino acid sequence.
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                                                 AAY79029 standard; protein; 728
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98US-0104834P.
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                                                                                                AAY79029;
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RESULT 3
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Sequence 728 AA;

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NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540
                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as meurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement of blood formation, e.g. after immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG
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                                                                                                                                                                                                                                                                                            Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood
                                                   /label= Differentiation_suppression_protein
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83.3%; Pred. No. 1.8e-190;
ive 47; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 77-82; 114pp; Japanese.
Location/Qualifiers
     /label= Signal
22. .723
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95JP-00311811
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Best Local Similarity
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                                                                                                                                 15-NOV-1996;
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30-NOV-1995;
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                                                                                                                                                                                                                             Sakano S,
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                                                                                                                      DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG
                                                                                                                                                                                                                             SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
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                                                                                           MGGR FLLTLALLSALLCRCQVDCSGVFELKLQEFVNKKGLLSNRNCCRGGCPGGAGQGQC
                                                                                                                                                                          FIWPGIFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY
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            Score 4108; DB 3;
Pred. No. 2.6e-225;
1; Mismatches 6;
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             98.98;
99.08;
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Best Local Similarity 99.0%
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leukaemia, malignant tumour.
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/label= signal
22. .723
/label= Delta-1
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                                                                                                                                                                                                                                                                                                                                                                        Human, delta-1 protein, ligand, notch, drug, vascular cell, primer, PCR, amplification.
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                                                                                                                                  LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
                                                                                                  EKYTEGONSOFPWIAVCAGIILVLMILLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN
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/note= "mature delta-1 protein"
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Best Local Similarity 83.3
Matches 609; Conservative
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EKDECVIATEV 723
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N-PSDB; AAX16817.
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Peptide Protein

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               SVKEEHGKCEAKCETYDSEAEEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
                                                                                                                              EKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHQPBACRSETETMNN
                                                      LANCOREKDISISVIGATOIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylation site"
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note= "N-myristoylation site"
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[abel= EGF-like_domain
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/label= Signal_peptide
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/note= "N
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/note= "T.
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/note= "h
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EKDECVIATEV 723
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                                                                                                                                                                                                                                                                             The present invention describes full length and shortened human delta-2 proteins. Human delta-2 is a differentiation inhibitor which inhibits the differentiation of undifferentiated cells (other than brain or muscle cells), such as blood cells, and enhances the proliferation of undifferentiated blood cells. Products of human delta-2 may be used for the treatment of diseases such as leukaemia and malignant tumours. They may also be used in the culture of human cells in vitro, e.g. for production of supplies of undifferentiated blood cells. The present electron example of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300
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                                                                                                                                                                                 Peptide inhibiting the differentiation of undifferentiated blood - used for treatment of cancer and other disorders and the culture of human cells in vitro.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.1%; Score 3494.5; DB 2
83.3%; Pred. No. 1.8e-190;
ive 47; Mismatches 64;
                                                                                                                                                                                                                                                            Example 1; Page 64-69; 86pp; Japanese
                                          98WO-JP002104.
                                                                      97JP-00124064.
                                                                                                   KASEI KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 609; Conservative
                                                                                                                                                         WPI; 1999-070120/06.
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                                                                                                                                                                       N-PSDB; AAX16300
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 723 AA;
                                                                                                 (ASAH ) ASAHI
                                          13-MAY-1998;
                                                                      14-MAY-1997;
               19-NOV-1998
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                                                                                           Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                              113
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                                                                                                                                                                                                                                                                                                                     Gape
              Ϋ́I,
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                                                                                                                                                                         Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers or breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia
              Wood
                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                       84.1%; Score 3494.5; DB 3; Length 723; 83.3%; Pred. No. 1.8e-190; ive 47; Mismatches 64; Indels 11;
              Napier M,
              Klein RD,
              Gurney AL,
                                                                                                                                                  Claim 12; Fig 8; 122pp; English.
                                                                                                                                                                                                                                                                                                      Best Local Similarity 83.34
Matches 609; Conservative
              Goddard A,
                                                      WPI; 2000-317943/27.
N-PSDB; AAZ93703.
                                                                                                                                                                                                                                                               Sequence 723 AA;
              Ashkenazi A,
                                                                                                                                                                                                                                                                                                                                                                                                    61
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'label= Prokaryotic membrane lipoprotein lipid attachment
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698. .702
/note= "Casein kinase II phosphorylation site"
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                                                                42. .346 -
note= "Casein kinase II phosphorylation
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note= "Casein kinase II phosphorylation
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                                                                                        43. .355
note= "Aen and Aep hydroxylation site"
44. .348
                                                                                                                                                                                                                                                                                      420. .432
/note= "Asn and Asp hydroxylation site"
                                                                                                                                                                                                                                                                                                                                                                      458. .480
/label= Asn and Asp hydroxylation site
467. -479
/label= EGF-like_domain
                                                     note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "N-myristoylation site"
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note= "N-myristoylation site"
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note= "N-glycosylation site"
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                           "N-myristoylation
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|abel= EGF-like_domain
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/label= EGF-like_domain
EGF-like domain
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/note= "cAMP and cGMP
phosphorylation site"
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/label= Fr<sup>7</sup>
57.
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/note= "Ca
495. .499
/note= "Ca
              128. .334
'note= "N·
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|abel= EC
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Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithyroid; antidabetic; noctropic; neuroprotective; antiansemic; hepatotropic; virucide; antipsoriatic; antialergic; antiasthmatic; hepatotropic; virucide; antipsoriatic; antiallergic; cotecoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; didopathic inflammatory myopathy; systemic sclerosis; sarcoidosis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; allergic disease; immune-mediated skin disease; allergic disease; immunelegical disease; allergic disease; immunelegical disease; allergic disease;
                                                                                                                                                                                                                                                                                                                                                     graft rejection; graft-versus-host-disease
                                                                                                                                                              Human PRO172 protein UNQ146 SEQ ID NO:41
                                                                                      AAB33422 standard; protein; 723 AA.
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99US-0131445P.
99US-0132371P.
99US-0134287P.
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99US-0123957P.
99US-0125775P.
99US-0128849P.
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06-JAN-2000; 2000WO-US000376
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EKDECVIATEV 723
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12-APR-1999;
20-APR-1999;
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14-MAY-1999;
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29-0CT-1999;
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30-NOV-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and anagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthitis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, sjogran's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune chromatory and transplantation associated diseases, including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of ruman PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                             Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                  KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Pan J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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11-FEB-2000; 2000WO-US003565.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
22-FEB-2000; 2000WO-US004414.
                                                                                                                                                                  Ashkenazi AJ, Baker KP,
Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
                                                                                                                      (GETH ) GENENTECH INC.
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N-PSDB; AAC58587.
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Sequence 723 AA;

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                        11; Gaps
84.1%; Score 3494.5; DB 3; Length 723;
83.3%; Pred. No. 1.8e-190;
ive 47; Mismatches 64; Indels 11;
             Best Local Similarity 83.3
Matches 609; Conservative
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   Query Match
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Best Local Similarity 83.3%;
Matches 609; Conservative
       2000-412154/35
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             N-PSDB; AAA77512
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diagnosis, trauma, wound, cancer, atherosclerosis, cardiac hypertrophy,
angiogenic, proliferative, cardiant, cardiovascular, antiatherosclerotic,
cytostatic, gene therapy, vaccine.
             SVKEEHGKCEAKCETYDSEAEEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
                                                                                                                                  CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
                                  NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT
                                                               EKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHOPEACRSETETMNN
                                                                      LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
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s. Paoni NF;
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Kuo SS,
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Klein RD,
Wood WI;
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                                                                                                                                                                                                                                                    Human PRO172 protein sequence
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99US-0115554P.
99US-0123957P.
99US-0131445P.
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99US-0141037P.
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14-MAY-1999;
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26-JUL-1999;
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13-8EP-1999;
15-8EP-1999;
15-8EP-1999;
05-OCT-1999;
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08-MAR-1999;
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovacular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, and conflowacularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NGs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24435 represent
Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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                                      Gaps
                                     11,
 Length 723;
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84.1%; Score 3494.5; DB 383.3%; Pred. No. 1.8e-190; ive 47; Mismatches 64;
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note= "Asx hydroxylation site"
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/label= EG
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                                                   593 LANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDT 652
                                                                                                                                                                                                                                                                                                                                   PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; melanoma; leukaemia; inflammatory disorder; angiogenic disorder; immunologic disorder; human.
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Jabel= EGF-like domain cysteine pattern signatu

    243. 255
    Abbel= EGF-like domain cystein pattern signatur

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note= "Tyrosine kinase phosphorylation site"
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/note= "N-myristoylation site"
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/label= Signal peptide
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; probetate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                          EKYTEGONSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNN
              LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
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18-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukemia and for identifying compounds capable of inhibiting growth of neoplastic cells.
                                            WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPPGFYGKICELSAMICADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Indels 11; Gaps
                                            Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 723;
                                            Napier MA,
                                           Gurney AL, Klein RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.1%; Score 3494.5; DB 3
83.3%; Pred. No. 1.8e-190;
ive 47; Mismatches 64;
                                                                                                                                                                                                                    Claim 31; Fig 8; 133pp; English.
                                           Ashkenazi AJ, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 83.3'
Matches 609; Conservative
             GENENTECH INC
                                                                                         WPI; 2000-638201/61.
                                                                                                        N-PSDB; AAAS4105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 723 AA;
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therapy; transgenic animal
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99US-0141037P.
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12-MAR-1999;
14-MAY-1999;
02-JUN-1999;
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08-SEP-1999;
15-SEP-1999;
15-SEP-1999;
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02-DEC-1999;
02-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANU12172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of actorogram from peripheral blood monocytes (PBMCS), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DRA, the release of properties probes, antisense RNA/DRA, the release of properties or the probes, antisense RNA/DRA, the release of the polymucleotides encoding probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FTWPGTFSLIIBALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY 173
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                                                                                                                             Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGSRCALALAVLSALL--CQVWSSGVFELKLQEFVNKKGLLGNRNCCR----GGAGPPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC
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                                                                                                                            Deforge L, Desnoyers L, Filvaroff E, G. A, Godowski PJ, Gurney AL, Sherwood S; Tumas D, Watanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Length 723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.1%; Score 3494.5; DB 4
83.3%; Pred. No. 1.8e-190;
ive 47; Mismatches 64;
                                                                                                                                                                                                                                                                                                   Claim 12; Fig 346; 813pp; English.
28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US023521.
23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
                                                                                                                                                                                                                                                                       breast, prostate, cervical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609; Conservative
                                                                                                                                           Goddard
                                                                                                                             Baker KP, Beresini M,
                                                                                                                                         Gerritsen ME, Goddard
Smith V, Stewart TA,
                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                    2001-408281/43.
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Best Local Similarity
Matches 609; Conserv
                                                                                                                                                                                                  N-PSDB; AAS21416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 723 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening;
CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                            354 CPPGFYGKICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSP
                                                                                                                                                                                                                  NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT
                                                                                                                                                                                                                                                                                                                           EKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHOPEACRSETETMNN
                                                                                                                                                                                                                                                                                                                                                       SVKEEHGKCBAKCETYDSBAEEK-SAVQLKSSDTSBRKRPDSVYSTSKDTKYQSVYVISE
                                                                                                          CANGAOCYDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                LANCOREKDISISVIGATOIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiogenesis-associated protein PRO172, SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB53064 standard; protein; 723 AA
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AABS3064-BS3097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, agonists of a RRO protein, fusion proteins comprising a PRO nucleic acid, the expression of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity, diagnoshing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue, treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid, or PRO indiced angiogenic disorder by detecting or stimulating endothelial cand methods of inhibiting or stimulating endothelial call growth, cardiac hypertrophy or PRO-induced angiogenist thereof administration of a PRO protein, or an agonist or antagonist thereof administration of a PRO protein, or an agonist or antagonist thereof cardiovascular, endothelial or angiogenic disorder, such as therefore and proteins, antibodies against pRO proteins, proteins, and proteins and the actoric and angential infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, Huntington's disease, or stroke. PRO proteins, a disease, or stroke. PRO proteins, and proteins, and in gene tecombinant production of PRO proteins, as hybridisation probes to make therapeutic agents. The present sequence represents a protein of the invention make therapeutic agents.

The present sequence represents a PRO protein of the invention
                                                                                                                                                                                                                 New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer.
                                              Goddard A;
ark MR, Marsters SA;
                                                KP, Ferrara N, Gerber H, Goddard A;
AL, Hillan KJ, Kuo SS, Mark MR, Ma
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                          Claim 69; Fig 2; 293pp; English
                                              Ashkenazi AJ, Baker KP,
Godowski PJ, Gurney AL,
(GETH ) GENENTECH INC.
                                                                                                                                                 2001-090793/10.
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                                                                                                                                                                         N-PSDB; AAC97368
                                                                                                 Paoni NF,
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61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY 173 SYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ 233 FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY 180 SYRPVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ 240 HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300 234 HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 293 1 MGSRCALALAVLSALL--CQVWSSGVFELKLQEFVNKKGLLGNRNCCR----GGAGPPPC 54 1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 11; Gaps DB 4; Length 723; 64; Indels 84.1%; Score 3494.5; DB 4 83.3%; Pred. No. 1.8e-190; ive 47; Mismatches 64; Query Match
Best Local Similarity 83.3
Matches 609; Conservative Sequence 723 AA; 241 55 121 181 174 114 ò g 8 8 ò g ઠે 셤 ઠે ठ

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98WO-US021141 98WO-US022991

17-SEP-1998; 07-OCT-1998; 29-OCT-1998;

301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT 360

98WO-US019437

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                                                CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                                                                                           CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
                                                                                                                           NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT
                                                                                                                                                                       EKYTEGONSOPPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHQPEACRSETETMNN
                                                                                                                                                                                                                    LANCOREKDISISVIGATOIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
                                                                                                                                                                                                                                                              SVKEEHGKCEAKCETYDSEAEEK-SAVOLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Juman; secreted and transmembrane protein; PRO; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted and transmembrane protein PRO172.
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                                                                                                                                                                                                                                                                                                                                                                                        ABO17788 standard; protein; 723
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98WO-US018824
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98WO-US014552
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22-MAR-2001; 2001US-00816794.
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10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00866216.

25-MAY-2001; 2001US-008660216.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001US-00866034.

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98WO-US022992.
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02-JUN-1999;
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01-MAR-2000;
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02-MAR-2000;
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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding col 275 nucleotide sequences, and which encodes a corresponding col 275 nucleotide sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a call expressing a PRO polypeptide, modulate a biological activity of a call, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine stimulate the release of proteoglycans, stimulate the binding of A-peptide conference of tumour in a mammal. The nucleic col factor VIIA, or detect the presence of tumour in a mammal. The nucleic colienses, premature aging, acquired immunodeficiency syndrome colinth defects, premature aging, acquired immunodeficiency syndrome collistications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating confidence of antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and collapsed to a collapsed to a collapsed to a novel human secreted and collapsed to a collapsed to a collapsed to a novel human secreted and collapsed to a collapsed 
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                  05-JUN-2001; 2001US-00874503.

14-JUN-2001; 2001US-0088634.

19-JUN-2001; 2001US-00886342.

20-JUN-2001; 2001US-00886342.

21-JUN-2001; 2001US-00807879.

22-JUN-2001; 2001WO-USO20116.

29-JUN-2001; 2001WO-USO20116.

09-JUL-2001; 2001US-00908827.

06-AUG-2001; 2001US-00924419.

09-AUG-2001; 2001US-00927795.

16-AUG-2001; 2001US-00927795.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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Best Local Similarity 83.31
Matches 609; Conservative
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N-PSDB; ACD24025.
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181 SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ 240

114 FTWPOTFSLIIEALHTDSPODLATENPERLISRLATORHLTVGEEWSQDLHSSGRTDLKY

173

FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY 180

DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG

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9705-0059352P
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9705-0062287P
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9705-0063752P
9705-0063124P
9705-0063127P
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9705-0063738P
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                                                                           HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSCT
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                                                                                                                                      CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                                                                      HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
                                                                                                                                                                                                        CANGAQCVDLGNSY1CQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
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tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
differentiation; chondrocyte; tumour; genetic disorder; cytostatic.
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98WO-US014552.
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98WO-US018824.
98WO-US019093.
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14-SEP-1998;
14-SEP-1998;
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20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUSBOR70-ABUSBIL44 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated PRO polypeptide useful for treating diabetes, rheumatoid archritis, sports injuries, obesity, hearing loss in mammals, stroke, heart attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-DEC-1999; 99WO-US028634.

02-DEC-1999; 99WO-US028651.

02-DEC-1999; 99WO-US028664.

02-DEC-1999; 99WO-US030095.

16-DEC-1999; 99WO-US030091.

20-DEC-1999; 99WO-US030091.

20-DEC-1999; 99WO-US03091.

30-DEC-1999; 99WO-US031274.

30-DEC-1999; 99WO-US030277.

06-JAN-2000; 2000WO-US000277.

06-JAN-2000; 2000WO-US000376.

11-FEB-2000; 2000WO-US000376.

11-FEB-2000; 2000WO-US000376.

18-FEB-2000; 2000WO-US000376.
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Smith V, Stewart TA,
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Best Local Similarity
Matches 609; Conserv
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02-MAR-2000;
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01-MAR-2001; 2001WO-US006520.
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14-MAR-2001; 2001US-00808689.
22-MAR-2001; 2001US-00816744.
05-MAR-2001; 2001US-00816744.
      99WO-US000106.
99WO-US005028.
99WO-US005190.
                      99WO-US008615.
99WO-US010733.
99WO-US012252.
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99WO-US020944.
99WO-US021090.
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99WO-US028409.
99WO-US028301.
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14-MAY-1999;
02-JUN-1999;
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05-JUN-2001;
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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for linking collocation of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The PRO polypeptides are useful for dentifying agonists or antagonists. The PRO polypeptides are useful for contained the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the proliferation or differentiation of sequences encoding PRO polypeptides are useful as hybridisation of chondrocytes, and detecting the presence of tumours. The polynucleotide sequences encoding PRO polypeptides, for generating transgenic animals or knockout animals, for the generation of antisenses RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation allysis of individuals with containing the properiors, for the generating transgenic canimals or knockout animals, for the generation canimals or knockout animals, for the generation canimals or knockout animals and the generation of animals animals and the sequence data for this patent was obtained in electronic format directly from the USPTO web site at sequence and sequence format directly from the uspto gov/psipadibles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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                                                                                                2001WO-US020116.
2001WO-US021066.
2001WO-US021735.
2001US-00908827.
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2001US-00927796.
2001US-00931836.
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  2001US-00882636
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                                                                     21-JUN-2001;
22-JUN-2001;
29-JUN-2001;
09-JUL-2001;
18-JUL-2001;
06-AUG-2001;
09-AUG-2001;
16-AUG-2001;
                          19-JUN-2001;
20-JUN-2001;
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11; Gaps 84.1%; Score 3494.5; DB 6; Length 723; 83.3%; Pred. No. 1.8e-190; tive 47; Mismatches 64; Indels 11; Query Match 84.1% Best Local Similarity 83.3% Matches 609; Conservative

61 DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120 FIWPGIFSLIIEALHIDSPDDLITENPERLISRLATORHLAVGEEWSODLHSSGRIDLKY 180 SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ 240 233 54 1 MGSRCALALAVLSALL -- CQVWSSGVFELKLQEFVNKKGLLGNRNCCR---- GGAGPPPC 1 MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC SYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY 121 114 181 174 셤 8 요 ò g ò 요 ò

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HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
    294 HHKPCKNGATCTNTGQGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCT
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Search completed: November 29, 2004, 13:21:52 Job time : 86.5563 secs

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November 29, 2004, 13:26:20 ; Search time 73.3366 Seconds (without alignments) 3520.994 Million cell updates/sec
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1 MGGRFLLTLALLSALLCRCQ.......YQSVYVISEEKDECIIATEV 728
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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                                                                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d					
Result		Query	Query				
No.	Score	Match	Length	DB	ΩI	Description	
-	4153	100.0	728	6	US-09-908-322-2	Sequence 2, Appli	
~	4153	100.0	728	10	US-09-783-931-2	Sequence 2, Appli	
m	4142.5	99.7	729	14	US-10-417-719-8	Sequence 8, Appli	
4	3495.5	84.2	721	σ	US-09-908-322-5	Sequence 5, Appli	
ß	3495.5	84.2	721	10	US-09-783-931-5	Sequence 5, Appli	
9	3495.5	84.2	721	15	US-10-042-865-109	Sequence 109, App	
7	3494.5	84.1	723	σ	US-09-828-366-21	Sequence 21, Appl	
80	3494.5	84.1	723	σ	US-09-995-593A-9	Sequence 9, Appli	
σ	3494.5	84.1	723	14	US-10-028-072-346	Sequence 346, App	
10	3494.5	84.1	723	14	US-10-140-808-346	Sequence 346, App	
11	3494.5	84.1	723	14	US-10-121-049-346	346,	
12	3494.5	84.1	723	14	US-10-123-904-346		
13	3494.5	84.1	723	14	US-10-140-470-346	Sequence 346, App	

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ALIGNMENTS

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TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                               CORRESONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LiP
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
STATE: NY
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: EstatsEQ Vergion 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Uul-2001
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                        APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, 8 Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
                   Sequence 2, Application US/09908322; Patent No. US20020107194A1; GENERAL INFORMATION:
US-09-908-322-2
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                                                                                                                                                                                                                     Query Match
100.0%; Score 4153; DB 9; Length 728;
Best Local Similarity 100.0%; Pred. No. 3e-266;
Matches 728; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                           ~
                                                                                               TYPE: amino acids
STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-908-322-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
                                         TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
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RESULT 2 US-09-783-931-2

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TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
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100.0%; Pred. No. 3e-266;
iive 0; Mismatches 0;
Sequence 2, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Teakonas, Spyridon
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-F6b-2001
CLASSIFICATION: UNKNOWN>
PRIOR APPLICATION: UNKNOWN>
PRIOR APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,605
REGISTRATION NUMBER: 32,605
REGISTRATION NUMBER: 32,605
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein SEQ ID NO: 2: US-09-783-931-2
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FABUSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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Best Local Similarity 100.
Matches 728; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                               181 SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
                                                                                                                241 HGFCDKPGBCKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQBGWGGLFCNQDLNYCT
                                                                                                                                                               HKRPCKNGATCTNTGGGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT
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                         SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
                                                                                          HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
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CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonda LLP
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESC Version 2.0
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/09/908,322
FILING DATE: 17-011-2001
CLASSIFICATION PATA:
CLASSIFICATION NUMBER: US/09/908,322
FILING DATE: 17-011-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09908322;
Patent No. US200207194A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Levis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
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CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                                                                                                                                                                                                                 LANCQREKDISISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSV
                                                       CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                                                                                                                           CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
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                                                                                                                                                                                               NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT
                                                                                                                                                                                                                                                                   EKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHOPEACRSETETMNN
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Pred. No. 1.5e-265;
0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/1041719
; Sequence 8, Application US/1041719
; Publication No. US20030180784A1
; GENERAL INFORMATION:
    APPLICANT: MILLEDMIUM Pharmaceuticals, Inc.
    APPLICANT: McCarthy, Sean
    APPLICANT: Gearing, David
    ITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
    FILE REFERENCE: MB101997-002CC2M
    CURRENT APPLICATION NUMBER: US/10/417,719
    CURRENT FILING DATE: 2003-04-17
    PRIOR APPLICATION NUMBER: US/09/568,218
    PRIOR FILING DATE: 1997-06-11
    SOFTWARE: FastSEQ for Windows Version 4.0
    SOFTWARE: FastSEQ for Windows Version 7.0
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llarity 99.9%;
Conservative
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ORGANISM: Gallus Gallus
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ECIIATEV 728
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Best Local Simi
Matches 728;
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LENGTH: 721 amino acids
                                                                             Sequence 5, Application US/09783931
Publication No. US20030073620A1
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10036/2711
COMPUTER ERADABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                      SEQUENCES:
712 KDECIIATEV 721
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Best Local Similarity
Matches 600; Conserva
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                                                                                                                                                                                                                                                      NUMBER OF
                                               RESULT 5
US-09-783-931-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 YSYRFVCDEYYYGEGCSDYCRPRDDAFGHFSCGEKGEKLCNPGWKGLYCTEPICLPGCDE 234
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                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                          Score 3495.5; DB 9; Lews-Pred. No. 9e-223;
                          TOTALLY TOTALLY IN CARGALIAN.

REGISTRATION NUMBER: 18,872

REGISTRATION NUMBER: 18,872

RELECCHANNICATION INFORMATION:
TELEPHONE: 212-790-909

TELEPHONE: 212-869-864

TELEPAX: 212-869-864

TELEPX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHRACATERISTICS:
LENGTH: 721 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                        65; Mismatches
                                                                                                                                                                                                                        TOPOLOGY: unknown

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-908-322-5
                                                                                                                                                                                                                  STRANDEDNESS: <Unknown>
                 ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                       84.2%;
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.2
Matches 600; Conservative
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CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF 119
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                                                                                                                               Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%; Score 3495.5; DB 10; Leliyu.
82.2%; Pred. No. 9e-223;
-- watematches 54; Indels
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Lewis, Julian Hart
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: INCOMPATION OF THE COMPUTER: DISACTOR OPERATING SYSTEM: DOS SOCIATOR DOS SOCIATOR DOS SOCIATOR DOS SOCIATOR DOS SOCIATOR APPLICATION DATA:

APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Peb-2001
CLASSIFICATION AUTHORN: AUTHORN: APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: ANTORNAYION SEGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELEPHONE: 212-790-909
TELEPHONE: 212-790-909
TELEPHONE: 212-790-909
TELEPHONE: 212-790-909
TELEPHONE: 212-790-909
TELEPHONE: 212-790-909
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLK 179
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                                                                                                                                                                                                                                                                                                                 Length 721;
                                                                                                                                                                                                                                                                                                                                          54; Indels
                                                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 82.2%; Pred. No. 9e-223;
Matches 600; Conservative 65; Mismatches 5
          CURRENT FILING DATE: 2002-05-17
CURRENT FILING DATE: 2002-05-17
PRIOR PELLING DATE: 2002-05-17
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-01-10
PRIOR PELLING DATE: 2001-01-10
PRIOR PELLING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR PELLING DATE: 2001-03-09
PRIOR PELLING DATE: 2001-03-09
PRIOR PELLING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SEQ ID NO 109
                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Xenopus laevis
US-10-042-865-109
   FILE REFERENCE: 21402-537
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APPLICANT: Malyankar, Uriel M
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John
APPLICANT: Smithson, Glennda
APPLICANT: Scuther, Exik
APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
                                                                                                                                                                         TCPPGFYGKNCELSAWTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS
                                                                                                                                   SCPPGFYGKNCELSAMTCADGPCFNGGRCADNPDGGYICPCPVGYSGFNCEKKIDYCSSN
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                HEGYCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC
                                                         THHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSC
                                                                           THHKPCENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDANPCKNGGSCSDLENSYTC
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Publication No. US20040029216A1
GENERAL INFORMATION:
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APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
APPLICANT: Shenoy, Suresh G
APPLICANT: Spylek, Kimberly
APPLICANT: Spylek, Kimberly
APPLICANT: Spylek, Kimberly
APPLICANT: Burgess, Catherine E
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M
APPLICANT: Taylor, Sarah
APPLICANT: Taylor, Sarah
APPLICANT: Taylor, Sarah
APPLICANT: Miller, Charles E
APPLICANT: Guo, Xiaojia
APPLICANT: Glodog, Ference L
APPLICANT: Alsobrook II. John P
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Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
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MacDougall, John
Malyankar, Uriel M
Mallet, Isabelle
Peyman, John
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KDECIIATEV 721
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                                                                                                                                               SVKEEHGKCEAKCETYDSEAEEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
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                                                 LANCOREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
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                                                                           DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG
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GENERAL INFORMATION, SELJI
APPLICANT: SAKANO, SELJI
FAPPLICANT: TOOH, AKIRA
TITLE OF INVENTION DIFFERENTIATION-SUPPRESSIVE POLY
FILLE REFERENCE: KP8447DIV
CURRENT APPLICATION NUMBER: US/09/995,593A
CURRENT FILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: UP/0-29611
FRIOR APPLICATION NUMBER: UP/-299611
FRIOR PILING DATE: 1998-06-18
FRIOR PILING DATE: 1995-11-17
FRIOR FILING DATE: 1995-11-17
FRIOR PILING DATE: 1995-11-30
FRIOR APPLICATION NUMBER: PCT/JP96/03356
FRIOR APPLICATION NUMBER: PCT/JP96/03356
FRIOR PILING DATE: 1996-11-15
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FRIOR PILING DATE: 1996-11-15
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FRIOR APPLICATION NUMBER: PCT/JP96/03356
FRIOR PILING DATE: 1996-11-15
FRIOR APPLICATION NUMBER: PCT/JP96/03356
FRIOR PILING DATE: 205611
FRIOR FILING DATE: 205611
FRIOR
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CRGANISM: Homo sapiens
US-09-995-593A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHKPCKNGATCTNTGQGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 CPPGFYGKICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSP 413
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APPLICANT: Achically, Avi
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Macin, Robert D.
APPLICANT: Wood, William I.
APPLICANT: Youn, Jean
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: MELGROWTH
FILE REFERENCE: PI6594RICI
CURRENT APPLICATION NUMBER: US/09/828,366
CURRENT FILING DATE: 2001-04-05
Prior filing data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 29
SEQ ID NOS: 29
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83.3%; Pred. No. 1e-222;
iive 47; Mismatches 6
                                                                                                                                                                         Sequence 21, Application US/09828366
Patent No. US20020010137A1
GENERAL INFORMATION:
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Best Local Similarity 83.3*
Matches 609; Conservative
                                                                                                                                                                                                                                                  APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Goddard, Audre
                                    KDECIIATEV 721
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US-09-828-366-21
  KDECIIATEV
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US-09-828-366-21
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PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064248
PRIOR APPLICATION NUMBER: 60/064809
PRIOR PELING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-12
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR PILING DATE: 1997-11-24
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R APPLICATION NUMBER: 60/063127
R FILING DATE: 1997-10-24
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R APPLICATION NUMBER: 60/073120

R FILING DATE: 1998-01-23

R FILING DATE: 1998-01-23

R FILING DATE: 1998-02-04

R APPLICATION NUMBER: 60/074086

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                                         FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062285
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/062287
FILING DATE: 1997-10-17
                        APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
FILING DATE: 1998-03-25
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FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
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APPLICATION NUMBER: 60/063045
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APPLICATION NUMBER: 60/063082
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APPLICATION NUMBER: 60/063561
FILING DATE: 1997-10-28
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APPLICATION NUMBER: 60/063733
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APPLICATION NUMBER: 60/063735
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APPLICATION NUMBER: 60/063738
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APPLICATION NUMBER: 60/063755
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1997-09-24
  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT PEPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-09-16
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-19
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
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APPLICANT: Bereeini, Maureen
APPLICANT: Berong, Laura
APPLICANT: Desnoyers, Laura
APPLICANT: Felvaroff, Ellen
APPLICANT: God, Wei-Qiang
APPLICANT: God, Wei-Diang
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Shewart, Timochy A.
APPLICANT: Yamas, Daniel
APPLICANT: Yamas, Daniel
APPLICANT: Zhang
TITLE OF INVENTION: TIME
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EKDECVIATEV 723
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US-10-028-072-346
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APPLICATION NUMBER: 60/079663 FILING DATE: 1998-02-27 APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-27

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                                                                                                                                                Gaps
                                                                                                                         DB 14; Length 723;
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                                                                                                                       84.1%; Score 3494.5; DB
83.3%; Pred. No. 1e-222;
ive 47; Mismatches 6
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR PILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR PILING DATE: 1998-07-07
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Best Local Similarity 83.3
Matches 609; Conservative
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Sequence 346, Application US/10140808; Publication No. US20030017563A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.

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DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 ACRIFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDG-GGADSAFSNPIRFPFG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCT 360
                                                                                                                                                      APPLICANT: SULLY, AUGUSTION STATEMENT: SULLY, AUGUSTION SUCH SULLY, AUGUSTION SUCKETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/121,049

CURRENT FILING DATE: 2002-04-12

PTION APPLICATION THEORY SECRET SULLY SAME CORREST AUGUSTION SULLY SULLY SAME SULLY SULL
601 LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
                               SVKEEHGKCEAKCETYDSEAEEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
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84.1%; Score 3494.5; DB 14; Length 723;

Best Local Similarity 83.3%; Pred. No. 1e-222;

Matches 609; Conservative 47; Mismatches 64; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 346, Application US/10121049; Publication No. US20030022239A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                        EKDECIIATEV 728
                                                                                                                                                                                                                                                                       ||||||:|||||
EKDECVIATEV 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapien
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                                     APPLICANT: Desnoyers.Luc

APPLICANT: Desnoyers.Luc

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gao, Wei-Qiang

APPLICANT: Godowski, Paul J.

APPLICANT: Godowski, Paul J.

APPLICANT: Sherwood, Steven

APPLICANT: Sherwood, Steven

APPLICANT: Shewart.Timothy A.

APPLICANT: Shewart.Timothy A.
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
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ORGANISM: Homo Sapien
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Best Local Similarity
Matches 609; Conserv
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11; Gaps

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DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120
                                                                                                                                                     481 NGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFT 540
                                                                                                                                                                                          MGSRCALALAVLSALL -- CQVWSSGVFELKLQEFVNKKGLLGNRNCCR----GGAGPPPC
                                         SYRFYCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ
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                                                                                                114 FTWPGTFSLIIEALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKY
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Filvaroff, Ellen
Gao, Wei-Giang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Peul J.
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Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Watanabe, Colin K
Wood, William
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EKDECVIATEV 723
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APPLICANT: Goddard, Audit b.
APPLICANT: Goddard, Audit b.
APPLICANT: Goddard, Audit b.
APPLICANT: Gorney, Audit b.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: And Cod, Wallliam
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1G54
CURRENT PILLING DATE: 2002-04-16
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                                          CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP
                                                                                                CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
LENGTH: 723
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Publication No. US20030022328A1
GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Bllen
APPLICANT: Gao, Wei-Glang
APPLICANT: Gerriteen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timcthy A.
APPLICANT: Stewart, Timcthy A.
APPLICANT: Tumas, Daniel
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EKDECVIATEV 723
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: 1933.0RTC160
CURRENT APPLICATION NUMBER: US/10/140,470
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
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                                                                                                                                                      DB 14; Length 723
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                                                                                                                                                    Query Match 84.1%; Score 3494.5; DE Best Local Similarity 83.3%; Pred. No. 1e-222; Matches 609; Conservative 47; Mismatches 6
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EKDECVIATEV 723
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                                                                                                         TYPE: PRT
ORGANISM: Homo Sapien
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US-10-140-470-346
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RESULT 14 US-10-175-746-346 ; Sequence 346, Application US/10175746

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                                                                                                                                                                                                                                                                                             APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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83.3%; Pred. No. 1e-222;
tive 47; Mismatches 6
                                                                                         Gao, Wel-Glang
Gerriteen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                     Watanabe, Colin K
Wood, William
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Best Local Similarity 83.3%
Matches 609; Conservative
                                                           Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                     Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-746-346
                                   APPLICANT:
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234 HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 293
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                                              294 HHKPCKNGATCINIGGGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCT
                                                                                       CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKK1DYCSSSP
                                                                                                      HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIBINECDANPCKNGGSCTDLENSYSCT
                                                                                                                                                               EKYTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHOPEACRSETETMNN
                                                                                                                                                 CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
                                                                                                                                                                                                                                                                                                                            LANCQREKDI SISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C3B ENCODING THE SAME
FILE REFERENCE: P3330R1C3B ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/176,918
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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 SYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQ
                                            LANCQREKDISISVIGATQIKNTNKKVDFHSDNS-DKNGYKVRYPSVDYNLVHELKNED-
                                                                                                      SVKEEHGKCEAKCETYDSEAEEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
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84.1%; Score 3494.5; DE
Best Local Similarity 83.3%; Pred. No. 1e-222,
Matches 609; Conservative 47; Mismatches 6
                                                                                                                                                                                                                                                                   Sequence 346, Application US/10176918
Publication No. US20030027275A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                APPLICANT: Bares, Kevin P.
APPLICANT: Beres, Kevin P.
APPLICANT: Beres, Kevin P.
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timcthy A.
APPLICANT: Tumas, Daniel
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EKDECVIATEV 723
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Best Local Similarity
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

November 29, 2004, 13:16:29; Search time 18.2447 Seconds (without alignments) 3839.238 Million cell updates/sec Run on:

US-09-783-931-2 4153 1 MGGRFLLTLALLSALLCRCQ......YQSVYVISEEKDECIIATEV 728 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

protein F11C7.4 [i preadipocyte facto delta-like homeoti glpl protein precu homeotic protein l slit-1 protein hom secreted leucine-r slit protein 2 pre slit protein 1 pre epidermal growth f EGF repeat transme hypothetical prote protein F40E10.4 [MEGFS protein - ra	intringic factor-B
289753 A54785 A54785 A32901 A32901 T42218 T42626 A36665 A3666 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A36665 A3666 A36665 A3666 A36665 A3666 A36665 A36665 A36665 A36665 A36665 A36665	T08618
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	45

ALIGNMENTS

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C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Gallus gallus (chicken)
C.Species: Ja-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C.Species: Ja-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C.Species: Ja-Sep-1996 #sequence_revision 15-NT99
R.Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
Nature 375, 787-790, 1995
A.; Title: Sxpression of a Delta homologue in prospective neurons in the chick.
A.; Reference number: ISO719; MUID:95319507; PMID:7596411
A.; Reference number: ISO719; MUID:95319507; PMID:7596411
A.; Residues: I-728 *HEN>
A.; Residues: I-728 *HEN>
A.; Residues: U-728 *HEN>
A.; Residues: U-729 *HEN>
A.;
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Gaps ö Length 728; Indels Query Match
100.0%; Score 4153; DB 2;
Best Local Similarity 100.0%; Pred. No. 3.3e-242;
Matches 728; Conservative 0; Mismatches 0;

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ò	7	MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 60	
qq	rt	MGGRFLLTTALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGFGGAGQQQC 60	
δ	61	DCKTFFRUCLKHYQASUSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFFG 120	0
ą	61	DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFG 120	0
δ	121	FTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSGRTDLKY 180	٥
qq	121	FINECTESLIEALHTDSPODLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKY 180	
ò	181	SYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQ 240	
qq	181	SYRFYCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEFICLPGCDEQ 240	0
ò	241	HGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCT 300	0
ą	241	HGFCDKPGECKCRVGWGGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNC	
ò	301	HHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSCT 360	
Dp	301	HHKP	0

CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420

301 361

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RESULT 3
JC7570
Delta Protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7570
A;Yoneya, T: Tahara, T: Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; A
J. Biochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a.new mouse and human notch ligand.
A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7570
A;Molecule type: mRNA
A;Residues: 1-685 < YONs
A;Cross-references: UNIPROT:Q9NR61; DDBJ:AB043894
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane recates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C;Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology
C;Keywords: transmembrane protein
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                                                                                                        TCPPGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSS
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                                                                                    TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS
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Best Local Similarity 48.2%; Pred. No. 1.1e-106;
Matches 352; Conservative 112; Mismatches 195; Indels
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EKDECVIATEV 722
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-101-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 148324
R; Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A; Title: Translant and restricted expression during mouse embryogenesis of Dll1, a murin A; Reference number: 148324; MUID:95401858; PMID:7671806
A; Accession: 148324
A; Mulcule type: mRNA
A; Scatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-722 ARES>
C; Genetics: C; Genetics: A; Gen
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  CPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSP 420
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                                                                       CANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGY
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;Superfamily: delta-4 protein; EGF homology
;331-362/Domain: EGF homology <EGF2>
;446-477/Domain: EGF homology <EGF>
;484-515/Domain: EGF homology <EGF>
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Best Local Similarity 79.5%
Matches 581, Conservative
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C,Species: Drosophila melanogaster
C,Bate: 20-eb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C,Accession: S19087
R;Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A,Reference number: S19087
A,Accession: S19087
A,Accession: S19087
A,Accession: Lega wins A,Accession: S19087
A,Accession: S19087
A,Accession: S19087
A,Accession: UNIPROF:P10041; EMBL:Y00222
C,Genetics:
   DEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDK
                   297 NGSTCSNSGPKGYTCTCLPGYTGEHCELGLSKCASNPCRNGGSCKDQENSYHCLCPPGYY
                                                                                                                                                                                                      PGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCK
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                                                                                                                          NGATCTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSCTCPPGFY
                                                                                                                                                                                      GKNCELSAMTCADGPCFNGGRCTD-NPDGGYSCRCPLGYSGFNCEKKI DYCSSSPCANGA
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larity 42.4%; Pred. No. 2.4e-86;
Conservative 83; Mismatches 241; Indels 73;
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C;Superfamily: neurogenic protein delta;
F;335-31/Domain: EGF homology «EGF1»
F;378-415/Domain: EGF homology «EGX1»
F;457-488/Domain: EGF homology «EGF3»
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Best Local S
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C;5569
Cspecies: Mus musculus (house mouse)
C;56cies: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;6ccession: JC7569
R;7coreya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; J.; Blochem. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Atle: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Accession: JC7569; MUID: 21064937; PMID:11134954
A;Accession: JC7569
A;Molecule type: mRNA
A;Residues: 1-686 < *YON*
A;Cross-references: UNIPROT:Q9DBU9; DDBJ;AB043893
C;Comment: This protein, a member of the Notch family of proteins, is a transmembrane re ates the Notch signaling, the growth or differentiation of vascular endothelial cells.
C;Genetics:
A;Gene: delta-4
C;Superfamily: delta-4 protein; EGF homology
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ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLPCNQDLNYCTHHKPCKNG
                                                                                                                       NCELSAMTCADGPCFNGGRCTD-NPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQC
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246
R;Kopczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes A;Mceference number: A31246, MUID:89196890; PMID:3149249
A;Mcession: A31246
A;Mcession: A31246
A;Mcession: A31246
A;Mcene: Testences: GB:Y00222
C;Genetics:
C;Genetics:
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VCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTF
                                                                                       EHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDKP
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85; Mismatches 240; Indels
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,Cross-references: FlyBase:FBgn0000463
;Superfamily: neurogenic protein delta;
;295-328/Domain: EGF homology <EGX1>
;422-450/Domain: EGF homology <EGF1>
;457-48/Domain: EGF homology <EGF>
;533-564/Domain: EGF homology <EGF>
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al Similarity 42.2%;
291; Conservative 89
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11 LLSALLC---RCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQCDCKTFFR

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Non-triple of the protein precursor - fruit fly (Drosophila melanogaster)
Nydremate names: gene D1 protein
Nydremate names: gene D1 protein
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S06670; A2637
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMBO J. 6, 3431-3440, 1987
A;Ritle: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic
A;Reference number: S0670
A;Accession: S0670
A;Accession: S0670
A;Accession: S0670
A;Residues: 1-880 <VAE>
A;Cross-references: UNIPROT:P10041; EMBL:X06289; NID:G7852; PID:G7853
A;Cross-references: UNIPROT:P10041; EMBL:X06289; NID:G7852; PID:G7853
A;Cross-references number: A31081; MUD:87218537; PMID:3107986
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and tA;Reference number: A31081; MUD:87218537; PMID:3107986
A;Residues: 422-436, ET', 439-458, 'A', 460-489, 'T', 491-621 <KNU>
A;Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KNU>
A;Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KNU>
A;Genetics:
A;Genetics:
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A;Genetics:
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A;Cross-references: PlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #satus predicted <SIG>
F;1-18/Domain: signal sequence #satus predicted delta protein #status predicted <MAT>
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;19-88/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                127 SLIVEAMH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCD 185
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A56136
R;Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notchl.
A;Reference number: A56136; MUID:95211842; PMID:7697721
                                                                                                                                                                                             :|||||||:
LCLKHYQATIDTTSQCTYGDVITFILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPGTF
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                                                                                                                     880;
                                                                                                                     Length
                                                                                                                                                  85; Mismatches 240; Indels
                                                                                                                     37.5%; Score 1555.5; DB 2; 42.2%; Pred. No. 4.4e-86;
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                                                                                                                    Query Match
Best Local Similarity 42.2
Matches 291; Conservative
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Gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: 316148; S16878; Ä3666
R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co-A;Accession: S16148
A;Accession: S16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 CKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 AWPRSYTLLVEA--WDSSND--TIQPDSIIEKASHSGMINPSRQWQTLKQNTGIAHFEYQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 GSCKLPGDCRCQYGWQGLYCDKCIPHPGCVHGTCNEPWQCLCETNWGGQLCDKDLNYCGT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NARSC-KNLIASYYCDCLPGWMGQNCDININDCLGQ-CQNDASCRDLVNGYRCICPPGYA 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 TWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 IRVICDDHYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECNKAICRQGCSPKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | | | : | | | : | | | 364 SPGWTGPTCSTNIDDCSPNNCSHGGTCQDLVNGFKCVCPPQWTGKTCQLDANECEAKPCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDHCERDIDECASNPCLNGGHCQNEINRFQCLCPTGFSGNLCQLDIDYCEPNPCQNGAQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GFCDKPGECKCRVGWOGRYCDECIRYPGCLHGTCOOPWOCNCOEGWGGLFCNODLNYCTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------BINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNCELSAMTCADGPCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 NGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDLGNSYICQCQAGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LALLSALLC -- RCOVDG - SGVFELKLOEFVNKKGLLSNRNCCRGGG -- -- PGGAGQQQCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 YRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQH
                                                                                                                                                                                                                                                                                                 Length 1220;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEI-------
                                                                                                                                                                                                                                                                                                 32.1%; Score 1332.5; DB 2; 41.9%; Pred. No. 1.5e-72;
                                                                                                                                                                                                                                                                                                                                                                                                        77; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Reaidues: 1-1351,'T',1353-1408 <THO2>
A;Cross-references: EMBL:X56811; NID:g8563; PID:g8564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 HERSNRYVCECARGYGGLNCQFL 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNRASDYFCKCPEDYEGKNCSHL 564
A;Residues: 1-1220 <LIN>
A;Cross-references: GB:L38483
F;379-410/Domain: EGF homology <EGF1>F;492-523/Domain: EGF homology <EGF2>F;634-665/Domain: EGF homology <EGF2>
                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 41.9%
Matches 236; Conservative
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us-09-783-931-2.rpr

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Accession: A35844
Status: preliminary; nucleic acid sequence not shown; not compared with conceptual trar;
Molecule type: mRNA
Residues: 1-2524 <COF>
Superfamily: Notch protein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                         : : : TCLCRPGYTGRLCDNDINECLSKPCLNGGQCTDRENGYICTCPKGTTGVNCETKI---- 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVSPEPPCTYGSAITPVLGANSFS--VPDGAGG-----ADPAFSNPIRFPFGFTWPGTF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLIIBALHT-------BPDDLTTENPERLISRLAT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DDCASNLCDNGKCIDKIDGYECTCEPGYTGKLCNININECDSNPCRNGGTCKD 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECESNP-CMMG----GTCKDMTGAYICTCKAGFSGPNCQTNINECSSNPCLNHGTCIDD 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---QQPWQCNCQEGWGGLFCNQD 295
                                                                         PDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNV 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xotch protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct_1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
   ECEAPHSAGIAANALLTTTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECRNQ
                                                                                                                                                                                                           DDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 CRCQVDGSGVP-BLKLQEFVNKKGLLSNRNCCRGGGGGGGGQQQCCKTFFRVCLKHYQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CICMPGYEGLYCETNIDECASNP-CLHNGKCI-----DKINEFRCDCPTGFSGNLCQHDF
                                                                                                                RFGHFTC-----CERGEKV-CNPGWKGQYC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DECTSTPCKNGAKCLD--GPNSYTCQCTEGFTGRHCEQDINECIPDPCHYGTCKDGIATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TEPICLPGCDEQHGFC-DKPGE--CKCRVGWQGRYC----DECIRYPGCLHGTC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.6%; Score 815; DB 2; Length 2524;
29.3%; Pred. No. 3.5e-41;
tive 68; Mismatches 220; Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRHLAVGEEWSQDLHSSGR-TDLKYSYRFVCDEHYYGEGCSVFCRPRD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: Ailtean Ciawed frog)
C;Species: Xenopus lacevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_ch
C;Accession: A35844
R;Coffman C:; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Ttle: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MuID:90385285; PMID:2402639
A;Accession: A35844; MuID:90385285; PMID:2402639
A;Accession: A35844; MuID:90385285; PMID:2402639
A;Accession: A35844; MuID:90385285; PMID:2402639
A;Residues: 1-2524 < COF
C;Superfamily: Notch protein; ankyrin repeat homology; EGF D;
C;Keywords: transmembrane protein
F;146-177/Domain: EGF homology <EGF>
F;184-125/Domain: EGF homology <EGF>
F;222-254/Domain: EGF homology <EGF>
F;185-487/Domain: EGF homology <EGF>
F;1924-1956/Domain: ankyrin repeat homology <ANI>F;1924-1956/Domain: ankyrin repeat homology <ANI>F;1927-1056/Domain: ankyrin repeat homology <ANI>F;2021-2023/Domain: ankyrin repeat homology <ANI>F;2021-2036/Domain: ankyrin repeat homology <ANI>F;2021-2036/Domain: ankyrin repeat homology <ANI>F;2027-2086/Domain: ankyrin repeat homology <ANI>F;2027-2086/Domain: ankyrin repeat homology <ANI>F;2027-2086/Domain: ankyrin repeat homology <ANI>F;2057-2089/Domain: ankyrin repeat homology <ANI>F;2057-2089/Doma
                                                                                                                                                                                                                                                                                                                                                    531
                                                                                                                                                                                                                                                                                                                                                                                              | | : | : | : | : | CHCPPDRAGKHCEQLRPLCSQPP 731
                                                                                                                                                                                                                                                                                                                                                    CECARGYGGLNCQFLLP---EPP
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Best Local Similarity 29.35
Matches 190; Conservative
              532
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R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Teakonas, S.
Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential
A;Reference number: A36666; MUID:91099666; PMID:2125287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 APDFTCDCAAGWTGPTCEINIDECAGGPCEHGGTCIDLIGGFRCECPPEWHGDVCQVDVN 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- ADGPCFNGGRCTDN 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFTWPGTFSLIIEAL---HTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DLKYSYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----TCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNCELSAM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 RITYRVRVQCAVTYYNTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCEEAICKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDEQHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQ-QPWQCNCQEGWGGLFCNQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDPVHGKCDRPGECECRPGWRGPLCNECMVYPGCKHGSCNGSAWKCVCDTNWGGILCDQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.1%; Score 1126.5; DB 2; Length 1408; Best Local Similarity 33.1%; Pred. No. 4e-60; Matches 226; Conservative 73; Mismatches 203; Indels 181;
                                                                                                                                                                                                                                                                                                                                                                         Constructions of the property 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phomology #status atypical <EG04>
F homology *EG05>
F homology *EG05>
F homology *EG08>
F homology *EG08>
F homology *EG08>
F homology *EG19>
F homology *EG11>
                                                                                                                                                                                                                                                                              PID:9158606
                                                                                                                                                                                                        Molecule type: mRNA
Residues: 1-15,20-26,'A',28-1408 <FLE>
Cross-references: GB:M35759; NID:g158605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNYCTHHKPCKNGATCTNTGQGSY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652-683/Domain:
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	PRESENT 12
Db 810 VAGYKCNCMLPYTGAICEAVLAPCAGSPCKNGGRCKESEDFETFSCECPPGWQGQTCEID 869 Qy 296 LNYCTHHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLEN 355 Db 870 MNECV-NRPCRNGATCONT-NGSYKCNCKPGYTGRNCEMDIDDCQPNPCHNGGSCSDGIN 927 QY 356 SYSCTCPPGFYGKNCELSAMTCAGPCFNGGTCDPDGGYSCRCPLGYSGFNCEKKIDY 415	RESULT 11 RESULT 11 RESULT 11 For a control of the control of t

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57,451-466,468-477,484-495/Disulfide bonds: #status predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-622
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Disulf
                                                                                                                                                                                                                           180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 GCSVFCRPRDDRFGHFTCGERGEK-----VCNPGWKGQYCTEPI-----CLPG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 --CDEQ-HGF----CDKPGE-----CDKPGE-------CKCRVGWQGRY 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747 IDECASMPCLNGGACIEMVN-GYTCQCVAGYTGVICETDIDECASAPCQNGGVCTDTING 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 866 SMPCQNGATCVNVGADYVCECVPGYAGQNCEIDINECASLPCQNGGLCIDGIAGYT--CQ 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREK 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGG----ADPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTTENP-ERLISRLATQ 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C----DECIRYPGCLHGTC---QOPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTN 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         629 CEINTDECASSPCMNGGLCVDQVNSYVCFCLPGFTGIHCGTEIDECA-SSPCLNGGQCID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 CONGGVCIDGVNGYMCDCQPGYTG--THCETDIDECARPPCQNGG-------DCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 GAVCVDGVNGFVCTCSAGYTGVLCETDINECASMPCLNGGVCTDLVNGYICTCAAGFEGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  514 NCET----DIDECASFPC-ONGAICIDOVNGYVCTCVPGYTGVLCEIDINECASFPCLNG
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                                                                                                                                                                                                                                                                                                                                                     Query Match 19.0%; Score 787.5; DB 2; Length 1064; Best Local Similarity 27.7%; Pred. No. 7.1e-40; Matches 211; Conservative 78; Mismatches 294; Indels 179;
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                       <EG15>
                                                                       <EG17><EG18><EG19><EG20>
                                                                                                                                                                         <EG21>
                  F/674-705/Domain: EGF homology ce F/712-743/Domain: EGF homology ce F/750-781/Domain: EGF homology ce F/788-819/Domain: EGF homology ce F/864-895/Domain: EGF homology ce F/902-933/Domain: EGF homology ce F/936-1064/Region: avidin-like
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ARSULT 14

ARSULT 14

ARSULT 15

ARSULT 15

ARSULT 15

ARSULT 15

ARSULT 16

C, Species : Strongylocentrotus purpuratus (purple urchin)

C, Species : Strongylocentrotus purpuratus (purple urchin)

C, Species : Strongylocentrotus purpuratus (purple urchin)

C, Accession: A40116; B40116; C40116; A39116; A41117

ARSULT 18

ARSULT 1
                                                                                                                                                                                                                                 997 CVTGYTGSNCQIEINECDSDPCENGATCQDRFGSYSCHCDVGFTGLNCEHVVQMCSPQNN 1056
SYSCTCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDY 415
                               CSSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCT 475
                                                                                                                                 CPPGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLP--EPPQG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;57-175/Domain: Clr/Cls repeat homology <C1R;
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F.218-249/Domain: EGF ht
F.256-287/Domain: EGF ht
F.294-32s/Domain: EGF ht
F.332-363/Domain: EGF ht
F.370-401/Domain: EGF ht
F.408-439/Domain: EGF ht
F.464-477/Domain: EGF ht
F.484-515/Domain: EGF ht
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Motch B protein - mouse (fragment)

N;Alternate names: Notch homolog

S;Specias: Mus musculus (house mouse)

C;Date: 21-3194 #sequence revision 05-Jan-1996 #text_change 16-Aug-2004

C;Accession: A49175; PHI570; 332113

R;Lardelli, M.; Lendahl, U.

R;Lardelli, M.; Lendahl, U.

A;Title: Motch A and Motch B-two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown
A;Ruceall type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:035516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g2879
A;Experimental source: embryo
A;Experimental source: embryo
A;Experimental source: embryo
A;Experimental source: embryo
C;Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision betwe
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F;143-174/Domain: EGF homology <EGX1>
F;560-591/Domain: EGF homology <EGX2>
F;674-705/Domain: EGF homology <EGX2>
F;712-743/Domain: EGF homology <EGX3>
F;836-867/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                      316 QGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNCELSAM 375
                                    772 INEFICHCPPGYTGKRCELDIDECSSNPCQHGGTCYDKLNAFSCQCMPGYTGQKCETNID 831
                                                                                                                                                                                                                                   456 SPPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NC----QPGTSG---LNCEINPDDCASN-----PCMHGVCVD---GINRYSCVCSP 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 G-----GADPAFSNPIR------FPFGFTWPGTFSLIIEALHTDSPDD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 LTTENP---ERLISRLATQRHLA----VGEEWSQDLH-----SSGRT--DLKYSYRFV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---shpcihgncigglsgykclcdagwydyncevdkneclsnpconggicnnlyngyrct 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 CDEHYYGEGCSV---FCRPR-----DDRFGHFTCGERGEKVCNPGWKGQYCTEPI- 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKKGFKGYNCQVNIDECASNPCLNQGTCFDDVSG-YTCH-----CMLPYTGKNCQTVLA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CLPGCDEQHGFC-DKPG----ECKCRVGWQGRYC----DECIRYPGCLHGTC---QQPW 279
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                                                                                                                  DCVTNPCGNGGTCIDKVNGYKCVCKVPFTGRDCESKMDPCASNRCKNBAKCTPSSNFLDF
                                                                                                                                                                                   45 NCCRGGGBGGAGQQCCDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGA
                                                                                                                                                            SCRCPLGYSGFNCEKKIDYCS-SSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCA
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                                                                                     376 TCADGPCFNGGRCTDNPDG------
                                                                                                                                                                                                                                                                                                           516 RGYGGLNCQ 524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --QCQAGTSGKNCEVNVNECHSNPCNNGATCIDGINSY------KCQCVPGFTGQHCE 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 EKVCNPGWKGQYCTEPI------CLPGCDEQHGFCDKPGECKCRVGWQGRYC- 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DECIRYPGCLHGTC---QQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;2538-2568/Region: glutamine-rich
F;2538-2568/Domain: neurogenic repetitive element #status predicted <OFA>
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Best Local Similarity 35.2%; Pred. No. 2.5e-39;
Matches 151; Conservative 52; Mismatches 139;
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Search completed: November 29, 2004, 13:26:58 Job time : 22.2447 secs

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Query Match
Best Local Similarity
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QBuwj4 brachydanio
Q6d48 brachydanio
Q7xxt xenopus lae
P79941 xenopus lae
P79941 mo sapien
Q91ac6 brachydanio
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Q9dbus mus musculu
G57409 brachydanio
Q6410 drosophila
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Aar21463 drosophil
Aar21463 drosophil
P10041 drosophila
Q6t4m9 drosophila
Q6t4m2 drosophila
                                                 November 29, 2004, 13:12:09; Search time 87.6462 Seconds (without alignments) 4779.132 Million cell updates/sec
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1 MGGRFLLTLALLSALLCRCQ.....YQSVYVISEEKDECIIATEV 728
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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DLL1_MOUSE
DLL1_RAT
QBUW74
QB0 148
QGD 148
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P79941
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DLL4 HUMAN
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1: uniprot_sprot:*
2: uniprot_trembl:*
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        drosophila

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ALIGNMENTS

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MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC 60
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Spinal cord;
MEDLINE-95319507; PubMed=7596411;
Hentique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz D.;
"Expression of a Delta homologue in prospective neurons in the
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 4153; DB 2;
larity 100.0%; Pred. No. 3.6e-268;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U26599; AAC59689.1; -.
PIR; I50719; I50719.
HSSP; P00740; IEDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:call communication; IEA.
InterPro; IPR00174; P:call communication; IEA.
InterPro; IPR00174; DSL.
InterPro; IPR00174; DSL.
InterPro; IPR001881; EGF 2.
InterPro; IPR001881; EGF II.
InterPro; IPR001881; EGF II.
PRT;
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                                            O1-NOV-1996 (TrEMBLrel. 01, C. 01-NOV-1996 (TrEMBLrel. 01, La 01-MAR-2004 (TrEMBLrel. 26, La C-Delta-1. Gallus gallus (Chicken).
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Pfam; PF00108; EGF; 6.
PRINTS; PR00010; EGFBLOOD.
SMART; SM0010; EGFBLOOD.
SMART; SM00179; EGF CA; 4.
PROSITE; PS00010; ASX HYDROXYL
PROSITE; PS001010; EGF 1; 9.
PROSITE; PS010186; EGF 2; 9.
PROSITE; PS010186; EGF 2; 9.
PROSITE; PS01187; EGF 2; 9.
PROSITE; PS01187; EGF 2; 9.
EGF-1;ke domain.
SEQUENCE 728 AA; 79861 MW;
PRELIMINARY;
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Nature 375:787-790(1995)
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GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLK 179
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"Primary neurogenesis in Xenopus embryos regulated by a homologue the Drosophila neurogenic gene Delta."; Nature 375:761-766\,(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.2%; Score 3495.5; DB 2; 82.2%; Pred. No. 2.1e-224; ive 65; Mismatches 54;
                                                   EMBL; L4229; AAC38017.1; -
HSSP; P00740; 1EDM.
GO; GO:0016509; C:membrane; IEA.
GO; GO:0015509; F:calcium ion binding; IEA.
GO; GO:0007154; P:call communication; IEA.
INTERPRO; IPRO0154; B:call communication; IEA.
INTERPRO; IPRO0144; DEC.
INTERPRO; IPRO0142; EGF 2.
INTERPRO; IPRO0184; EGF 1.
INTERPRO; IPRO0189; EGF 1.
INTERPRO; IPRO0189; EGF 1.
INTERPRO; IPRO0189; EGF 1.
PFam; PF00109; EGF 1.
PFAM; PF00109; EGF 1.
PROSITE; PS00010; EGF 6.
PROSITE; PS0010; ASX HYDROXL; 3.
PROSITE; PS01186; EGF 7; 8.
PROSITE; PS01186; EGF 7; 8.
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EGF-11ke domain.
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091902, 0191902, 0191902, 010 Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 26, Last annotation update)
X-Delta-1. 26, Last annotation update)
X-Ronopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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SEQUENCE FROM N.A.
MEDLINE=95319503; PubMed=7596407;
Chitnia A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;
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NCBI_TaxID=8355;
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                                  SVKEEHGKCEAKCETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEE
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
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"Human ligands of the Notch receptor.";
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MEDLINE-22897296; Pubmed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
Chow B., Chui C., Crowley C., Currell B., Douel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
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Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,
Henrique D., Parreira L.;
"Differential effects of Notch ligands Delta-1 and Jagged-1 in human
lymphoid differentiation.";
J. Exp. Med. 194:991-1001(2001).
-i. FUNCTION: Acts as a ligand for Notch receptors. Blocks the
differentiation of progenitor cells into the B-cell lineage while
                                                                                                                                                               000548; Q9NU41; Q9UJV2;
115-JUL-1998 (Rel. 36, Created)
115-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal)
(H-Delta-l) (UNQ146/PR0172).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment.";
                                                                                                                                                                                                                                                                                                                                                                                                       Han W., Ye Q., Moore M.A.S.;
"A soluble form of human delta-like-l inhibits differentiation of hematopoietic progenitor cells.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                              Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Almeida J.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
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Mammalia; Eutheria; Primates;
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1. SUBDAIT: Interactes with Noth Treeporce.

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                         SVKEEHGKCEAKCETYDSEAEEK-SAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISE
                                        FRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPG
593 LANCQREKDISVSIIGATQIKNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDT
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                                                                                                                                                                                                                                                               Cynops pyrrhogaster (Japanese common newt).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
NCBI_TaxID=8330,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 726;
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                                                                                                                                                                                                                                                                                                                                           Saito T.;
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352A40219AE67F41 CRC64;
                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Ligand Delta-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.1%; Score 3449.5; DB 2; 83.2%; Pred. No. 2.5e-221; ive 46; Mismatches 69;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Nakamura K., Kikuchi Y., Susaki K., Chiba C.,
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ
-!- SMILARITY Contains 8 EGF-like domains.
EMBL, SAB095017, BAC41350.2;
--- HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; D00740; LEDM.

GO; GO:0016620; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0007154; P:call communication; IEA.
InterPro; IPR00152; Asx_hydroxyl_S.
InterPro; IPR001742; EGF_Z.
InterPro; IPR001841; EGF_Z.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
InterPro; IPR006209; EGF_II.
Ffam; PF010144; DSL; 1.
Pfam; PF010144; DSL; 1.
Pfam; PF001010; EGFBLOOD.
SMART; SM00011; EGF; 6.
BRINTS; PR00110; EGF 6.
SMART; SM00119; EGF 7.
                                                                                                                                                                        Z
                                                                                                                                                                      726
                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00010; ASX HYDROXX
PS00022; EGF_1; 8.
PS01186; EGF_2; 7.
PS50026; EGF_3; 6.
PS01187; EGF_CA; 2.
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nes 603; Conservative
                                                                             EKDECIIATEV 728
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EKDECVIATEV 723
                                                                                                                                                                      PRELIMINARY;
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EGF-like domain
                                                                                                                                                                                                                                                  Name=Delta-1
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01-MAR-2003
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                                                                                                                                                                                                                                                                           -linked (GlcNAc. . .) (Potential)
-> Q (in Ref. 2).
-> R (in Ref. 2).
-> S (in Ref. 2).
B4EC455FR32A12B CRC64;
                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 3487.5; DB 1; Length 723; 83.2%; Pred. No. 7.3e-224; ive 47; Mismatches 65; Indels 11;
 By similarity.
                                               Best Local Similarity 83.2
Matches 608; Conservative
 174
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DISULPID
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[5]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
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SEQUENCE FROM N.A.
                       Proc. Natl. Acad.
                                                                                                                                                                 STRAIN=C57BL/6J;
                                                                                                                      Strausberg R.
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STRAIN-C57BL/6; TISSUB-Mouse;

KATAIN-C57BL/6; TISSUB-Mouse;

KATAIN-C57BL/6; TISSUB-Mouse;

KATAIN-C57BL/6; TISSUB-Mouse;

KATAIN-C57BL/6; TISSUB-Mouse;

KATAIN-C57BL/6; TISSUB-Mouse;

KATAIN-C57BL/6; PubMed-12477932;

KATAIN-C57BL/6; May G. May G. M., Schuler G.D.,

Altschul S.F., Zecherg B., Buetow K.H., Schnefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

LA Brownstein M., Soarse M.B., Bonaldo M.F., Carainci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gany L.J., Hulyk S.W.,

KIChards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachards S., Mothey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E.,

J. Jones S.J., Marra M.A.;
                                                                                                          425
                                           301
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                                                                                                                    QCVDIGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNC 485
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                                                                                                                                                                                                                                       GONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQK-RHHQPEACRSETETMNNLANC 604
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                                                                                                                                                                                                                                                                                                                                      STPVSRCEHSPCHNGATCHERNNRYVCECARGYGGLNCQFLLPEQPQEHDTGDNTEKYTE
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                     KPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC
                                                               KNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGF
                                                                                                          YGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGA
                                                                                                                                                                                             STPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEKYTE
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              722 AA
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05-JUL-2004 (TrEMBLrel. 27, C:
05-JUL-2004 (TrEMBLrel. 27, L:
01-OCT-2004 (TrEMBLrel. 28, L:
Delta-like 1
Name=Dll1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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"Generation and initial analysis of more than 15,000 full-length human
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BY STRAINGENEY JELOGIA

SUBMITTED CONTAINS B EGF-11ke domains.

EMBL; BCO5740013 to the EMBL/GenBank/DDBJ databases.

C. 1 SINTALARITY: Contains B EGF-11ke domains.

EMBL; BCO57400 AAH57001; --

EMBL; BCO57400 AAH57001; --

EMBL; BCO57603; AAH55063.1; --

EMBL; BCO57603; AAH55063.1; --

EMBL; AY497019; AR30869.1; --

EQ; GO:0007386; P: promptre specification; IMP.

EQ; GO:0007386; P: promptre specification; IMP.

EN INTERPO: IPRO00189; EGF_11.

EN ENTERPO: IPRO00189; EGF_11.

EN ENTERPO: IPRO00189; EGF_11.

EN EMART; EMPOO143; EGF_2.

EN EMART; EMPOO109; EGFE_0.

EN EMART; EMPOON EN EMPO
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                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brathwaite M.E.;
the EMBL/GenBank/DDBJ databases
                                                                                    Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-MOUBe;
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                                                 cDNA sequences.
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Submitted (DEC-2003) to
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GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLK 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THHKPCKNGATCTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSC
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                                                                                                                                                                                                                                                                           722;
                                                                                                                                                                                                                                                                       Query Match 82.1%; Score 3410; DB 2; Length 7
Best Local Similarity 79.5%; Pred. No. 1.1e-218;
Matches 581; Conservative 72; Mismatches 66; Indels
                                                                                               Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC057400; AAH57400.1; -. SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
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[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
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STRAIN=C57BJ/6; TISSUB=Mouse;

MEDLINE=233825; PubMed=1247,932;

MEDLINE=233825; PubMed=1247,932;

A Straubberg R.D., Peingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hshah F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakarn P.J., McKernan K.J., Malek J.A., Gunsaratne P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A.M., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Sha Marra M.A.,

"Mones S.J., Marra M.A.,

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       QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC
                                          SERHMESQGGPFPWVAVCAGVVLVLLLLGGAAVVVCVRLKLQKHQPPPEPCGGETETWN
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                                                                                                                                                                                                        THHKPCRNGATCTNTGGGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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AAH57400;
02-MAR-2004 (TEMBLEE]. 27,
02-MAR-2004 (TEMBLEE]. 27,
02-MAR-2004 (TEMBLEE]. 27,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                     722 AA
                                                                                                                                                                                                                                      Created)
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STRAIN=C57BL/6; TISSUE=Mouse;
                                                                                                                                                                                                                               02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.
          EKDECVIATEV 722
                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              Delta-like 1.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QHGFCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYC 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL 531
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DLLI.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 722;
                                                                                                                                                                                                                               STRAIN=CS7BL/6J;
agaraja R., Waeltz P., Brathwaite M.E.;
"Genomic Sequece Analysis in the Mouse t-complex Region.";
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY497019; AAR30869.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.1%; Score 3410; DB 2; 79.5%; Pred. No. 1.1e-218; ive 72; Mismatches 66;
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Matches 581; Conservative
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                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
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EMBL; X80903; CAA56865.1;
PIR; 148324; 148324.
HSSP; P00740; 1EDM.
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                       419
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                                                                PCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPG 479
                                                                            480 YNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF 539
                                                                                                                      472 YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGGGGGPNCQFLLPEPPPGPWVVDL 531
                                                                                                                                                    540 TEKYTEGONSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVOKRHHQPEACRSETETMN 599
                                                                                                                                                              NLANCOREKDISISVIGATQIKNTNKKVDFHSDN-SDKNGYKVRYPSVDYNLVHELK-NE 657
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                       TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6 X BALB/c; TISSUB=Embryo;
MEDLINE=95401858; PubMed=7671806;
Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
"Transient and restricted expression during mouse embryogenesis of D111, a muxine gene closely related to Drosophila Delta.";
Development 121:2407-2418(1995).
                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system. SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: In the embryo, expressed in the paraxial mesoderm and nervous system. Expressed at high levels in adult heart and at lower levels, in adult lung.
DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo. Expression then decreases and increases again in the adult. SIMILARITY: Contains 8 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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EKDECVIATEV 722
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                CACRTFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGA-GIDPAFSNPIRFPF
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                                        Gaps
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p97677;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1)
Name=Dll1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                        12;
.) (Potential)
                        Length 722;
                       82.0%; Score 3407; DB 1; Length 7; 79.5%; Pred. No. 1.7e-218; ive 71; Mismatches 67; Indels
   N-linked (GlcNAc.
                                       Matches 581; Conservative
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EKDECVIATEV 722
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Bubbaited (DEC-1956) to the Pseu/Goedent/Dong detachases.

- In Summarian embryos. May have a role in callular interactions command the process of the callular interactions of the management of the nervous system (By smallarty) and contained the process of the callular interactions of the management of the nervous system (By smallarty) and contained the process of the callular interaction of the management of the nervous system (By smallarty) and contained the process of the callular interaction of the system and the Smallarty of the State Interaction of the Surgeoment (San June 1997) and the Surgeoment of the interaction of the Surgeoment (San June 1997) and the Surgeoment of Surgeoment of Surgeoment of the Surgeoment of the Surgeoment of Surgeoment
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ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNG 308
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDINIBE-22248969; MEDINIBE-22248969; bubMed=12361969; Mans S., Campos-Ortega J.A.; Mans S., Campos-Ortega J.A.; "On the organisation of the regulatory region of the zebrafish deltad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDKPG
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                                                                                                                                                                                              01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Caniata, Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Bewelopment 129:4773-4784(2002).

Bewelopment 129:4773-4784(2002).

Bewelopment 129:4773-4784(2002).

Go; Go:001600; E:cellcium ion binding; IEA.

Go; Go:001569; F:cellcium ion binding; IEA.

Go; Go:001569; F:cellcium ion binding; IEA.

Go; Go:001569; F:cellcium ion binding; IEA.

InterPro; IPR001174; DSL.

InterPro; IPR001174; EGF_Z.

InterPro; IPR00181; EGF_I.

InterPro; IPR00181; EGF_I.

Fram; PF001414; DSL; 1.

PFam; PF001019; EGF_I.

PFAMT; SM00179; EGF_I.

SWART; SM00179; EGF_I.

PROSITE; PS01186; EGF_I; 8.

PROSITE; PS01186; EGF_I; 8.

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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 3354; DB 1;
; Pred. No. 5.6e-215;
69; Mismatches 69;
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78.4%;
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                                                                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                          2; Length
                                                                                                                                                                                                                                                                                                73.7%; Score 3061.5; DB 2; Length llarity 73.3%; Pred. No. 1.7e-195; Conservative 81; Mismatches 95; Indels
PROSITE; PS00010; ASX HYDROAll; J. PROSITE; PS00022; EGF_1; 8. PROSITE; PS00186; EGF_2; 8. PROSITE; PS00187; EGF_3; 6. PROSITE; PS101187; EGF_3; 6. PROSITE; PS101187; EGF_GA; 2. EGF-like domain; Signāl; Transmembrane.

SIGNAL 4 11 Potential.

717 AA: 79061 MW; 9C5A0162504593E4 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name=dld; Synonyms=deltaD;
Name=dld; Synonyms=deltaD;
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBI_TAXID=7955;
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MEDLINE-97ACH.

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MOST CAMPOO-OKTEGA J.A.;

MOST CAMPOO-OKTEGA J.A.;

MOST CAMPOOLED OF THE DESCRIPTION OF DETHNARY NEURONS and Sommer and Sommer.

MEDLINE-97ACH.

MEDLINE-97AC
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Pfam; PF001009; BGF; 6.
PRINTS; PR0010; EGFBLCOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; BGF_CA; 4.
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P87357
DD P87359
DT 01-MA
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248

239

128 119 188 179

68 61 308

299 368 359 428 419 488 546

605 598 665

688

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NGARCVDLVNSYLCQCPDGFTGMNCDRAGDECSMYPCQNGGTCQEGASGYMCTCPPGYTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                705 YSESRYSESKYSESKYSDVSLYSESACASACASASTSACVDTKYKSVMVMSEEKD 764
                                                                                                                                                                                                                                                                                                                                             645 VKFEVKHEVKLEHAGKETTMANELSDSCEDIKCOSLODSSECTEEKRRKRLKSDASEKSK 704
                                          KNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEK
                                                                   543 YTEGONSOFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQ--KRHHQPEACRSETETMNN
                                                                                                                                                     -----SDVPWTAVGSGVLLVLLVVACAVVVVCVRSKVQQRRRDEDEVANGENETINN
                                                                                                                                                                                                                LA-NCQREKDISISVIGATQIKNTNKKVDFHSDNSD-----KANGYKVRYPSVDYNLVHE
                                                                                                                                                                                                                                        LKNE--DSVKEEH-GK------CE-AKCETYDSEA---EEKSAVQLKS-----
                                                                                                                                                                                                                                                                                                                                                                                          ---SDTSERKRPDSVYSTSK-------DTKYQSVYVISEEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-dla; Synonyms-deltaA;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDIATE-98165193; MEDIATE-98165392; PubMed=9425133; Appel B., Eisen J.S.; "Regulation of neuronal specification in the zebrafish spinal cord "Regulation of neuronal specification in the zebrafish spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0D8A9734585918E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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BMBL; AF030011; AAC41249.1; -.

BMBL; AF030011; AAC41249.1; -.

HSSP; P00740; 1EDM.

ZFIN; ZDB-GENE-980526-29; dla.

GO; GO:0016020; C: membrane; IEA.

GO; GO:0005209; F: calcium ion binding; IEA.

GO; GO:0007154; P: calcium ion binding; IEA.

InterPro; IPR00174; P: calcium ion binding; IEA.

InterPro; IPR00174; BSE.

InterPro; IPR00143; EGF_Ca.

InterPro; IPR00143; EGF_Ca.

InterPro; IPR00143; EGF_II.

InterPro; IPR00143; EGF_II.

InterPro; IPR00143; EGF_II.

Pfam; PF00008; EGF_I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0010; EGFBLOOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF CA; 3.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antechnic L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toonhyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., WcKernan K.J., Malke J.A., Gunarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevychenko Y., Bouffard G.G.,
M. Richards M.M., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.J.,
Jones G.J., Marra M.J.,
Jorder G.J., Marra M.J.,
Jones G.J., Marra M.J.,
Jones G.J., Marra 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTFFRICLKHYOPNASPEPPCTYGGTVTPVLGSNSFQVPDTL--PDGSFTNPIRMNFGFT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 WPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 WPGTFSLIIEALHADSKEDLTTENPERIISTWTTQRHLTVGEDWSQDLHSVGRTELKYSY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHG 242
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             Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.3%; Score 2918.5; DB 2; Length 772; 65.5%; Pred. No. 6e-186; ive 77; Mismatches 116; Indels 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Embryo;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO15742; AAH75742.1; -.
Hypothetical protein.
SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                       TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA sequences.
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  Hypothetical protein
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Best Local S:
Matches 516
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                                       15;
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                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                          242
                                                                                                                                                                                                                                                                                                                                                                               362
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SDVPWTAVGSGVLLVLLLVVACAVVVVCVRSKVQQRRRDRBDEVANGENETINN 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEK 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LA-NCOREKDISISVIGATQIKNTNKKVDFHSDNSD-----KNGYKVRYPSVDYNLVHE 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKNE--DSVKEEH-GK-----CE-AKCETYDSEA---EEKSAVQLKSSDTSERK 695
                                                                                                         97
                                                                                                                                           KTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFT
                                                                                                                                                             3 GRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQCDC
                                                                                            || || || || SILYMELCQASSSGVFELKLQEFLNKKGVQGNKNCCKGGLT--TSYQQCEC
                                                                                                                                                                                                                 WPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY
                                                                                                                                                                                                                                    RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHG
                                                                                                                                                                                                                                                                                                                                                             FCDKPGECKCRVGWQGRYCDECIRYPGCLHGTCOOPWOCNCOEGWGGLFCNODLNYCTHH
                                                                                                                                                                                                                                                                                                                                                                                                                                KPCKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 YTEGONSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQ--KRHHQPEACRSETETMNN
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MGC52561 protein.
MGC5261 protein.
Kenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                       53;
 Length 802;
   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPDSVYSTSK--DTKYQSVYVISEEK-DECIIATEV 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          743 YSESRYSESKYSESKY----SESKYSRCIAVFRV 772
                        1.1e-181;
68.7%; Score 2854.5;
66.4%; Pred. No. 1.1e-
ive 78; Mismatches
                  Local Similarity 66.4
nes 502; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355,
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                                                                                                                                           63
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 Query Match
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Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Brange C.,
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Rakeley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO44262; AAH44262.1; -.
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M-delta-1 polypeptide (AAW11720) is the mouse homologue of Drosophila Delta, a protein that binds to Notch protein. It is expressed primarily in presomitic mesoderm, the central and peripheral nervous systems, and kidney. Chick (AAW11719) and human (AAW11721-38) Delta-1 polypeptides have also been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, as well as nervous system disorders, and to promote tissue regeneration and repair
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preventing cancer, nervous system disorders and for tissue regeneration.
                                                                                                                                                                                                                                                                  M-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma; neurogenesis; therapy.
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        Length 722;
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       Score 4007; DB 2;
Pred. No. 2.2e-225;
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Query Match
Best Local Similarity 97.45
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Mouse notch ligand delta-like 1 protein. ABU55873 standard; protein; 722 AA. (first entry) 25-MAR-2003 ABU55873; RESULT 2 ABU55873

97.1%;
Best Local Similarity 97.2%;
Matches 702; Conservative Sequence 722 AA; Notch; Wnt; embryonic stem cell; embryogenesis; human; differentiation; ligand; Parkinson; disease; Huntington's disease; motor neuron disease; heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

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Gaps

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Length 722; Indele

Score 4003; DB 6; Pred. No. 3.7e-225; 4; Mismatches 16;

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The invention relates to modulating the differentiation of an embryonic catem cell, comprising: (a) providing a culture of embryonic stem cells; (c) by providing at least one ligand or its active binding fragment, capable of binding at least one ligand or its active binding fragment, capable of binding at least one ligand or least seed to be binding at least one ligand or least seed to be binding at least one ligand, and (d) forming a culture comprising embryonic stem cells and the ligand, and (d) growing the cell culture. Also included are: (i) any of 9 fully defined with a nucleic acid molecule selected from: (i) any of 9 fully defined with a nucleic acid molecule selected from: (i) any of 9 fully defined with a nucleic acid molecule which are dependented as a result of the genetic code to code any of a ligand capable of binding a whr receptor; or (iii) mucleic defined which are degenerated as a result of the genetic code to the sequences of (i) or (ii) (b) forming a culture comprising the cell deferentiation of the embryonic stem collure for the maintenance and/or differentiation of the embryonic stem cells; (a) providing at the differentiation of the embryonic stem cell; and (c) growing the cell identified in (a) with an embryonic stem cells, comprising the cell identified in (a) with an embryonic stem cells; and (c) growing the cell identified in (a) with an embryonic stem cells, comprising; (a) providing a cell transfected with a nucleic acid molecule selected from: (i) a molecule encodes a polypeptide capable of inhibiting the differentiation of embryonic stem cells; on the and molecule selected from: (i) and encodes a polypeptide capable of inhibiting who signalling; on (ii) nucleic acid molecule selected from: (i) becaming a culture contained state, and (ii) nucleic acid molecule selected from: (i) becaming a cell transference of embryonic stem cells; comprising the cell identified in (a) with an embryonic stem cells; on undifferentiated state, and (ii) or (ii); hording a providing a cell comprising ad
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                                                                                                                                                                                                                                                                                                                                                                                                                    Modulating the differentiation of embryonic stem cells by providing ligands which bind receptors in the Notch and Wnt pathways, useful ftreating diseases such as Parkinson's, Huntington's, heart disease,
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23-MAR-2001; 2001GB-00007299.
17-APR-2001; 2001GB-00009346.
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                                         WO200277204-A2
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29-APR-2002; 2002WO-GB001946
                            (AXOR-) AXORDIA LTD
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Best Local Similarity
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The present invention relates to a novel screening method which enables the identification of biologically active agents which mediate their the identification of biologically active agents which mediate their effect through the activation of genes. The method involves providing a population of cells stably transfected with a nucleic acid encoding a reporter molecule, cloning the transfected with a nucleic acid encoding a reporter molecule, cloning the transfected cells into a cell array, crossing the array to at least one agent to be tested and detecting a signal generated by the reporter molecule as a result of exposure to the gent. The method is useful in identifying biologically active agents and the genes through which the agents act, in screening potential drugs for their ability to activate certain drug targets in a high-throughput assay, in identifying relationships between signalling pathways and specific signals that could be useful in eventually directing the could be useful in eventually directing the testing for unwanted activation or inhibition of genetic signalling pathways. The present sequence is murine notch ligand delta-like I protein used to illustrate the method of the invention
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Pred. No. 3.7e-225;
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97.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exposure to the agent.
                                                                                                                                                      Draper J,
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N-PSDB; AAD52523.
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us-09-783-931-12.rag

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cc mucleic acid or its antibody, the activity or levels of delta protein is modulated and vice versa. A delta cleavage poptide or its derivative capable of binding kuz protein is useful for treating or preventing a disease or disorder associated with increased delta activity or expression such as cervical, breast, colon or lung cancer, melanoma or eseminoma in humans. A recombinant cell comprising a delta peptide is useful for treating or preventing central nervous system disorders. A cleavage peptide is useful for the diagnosis of diseases or disorders associated with increased levels of Notch-delta protein binding activity comprising measuring the ability of delta cleavage peptides in a cativity comprising measuring the ability of delta protein and kuz is useful complex, complex or screening for the presence of, or predisposition to developing a disease or disorder associated with aberrant levels of the complex, comprising measuring the level or functional activity of the complex or RNA encoding delta or kuz in a sample. The delta cleavage peptide is also useful for promoting tissue regeneration and repair, for treating liver cirrhosis, keloid formation, psoriasis, baldness and degenerative or traumatic disorders of the sensory epithelium of the
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                                             VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG
                                                                                                                                                                                                                                    GPPPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPPPCGGETETMNNLANCQREK
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                                                                                      MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR
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                          Length 722;
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                          96.0%; Score 3955; DB 3;
96.1%; Pred. No. 2.3e-222;
ive 6; Mismatches 22;
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Matches 694; Conservative
Sequence 722 AA;
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This sequence represents the murine delta protein amino acid sequence. Delta is a toporythmic protein that contains a sequence which is cleaved by the metalloprotease-disintigin Kuzbanian (Kuz). Cleavage by Kuz results in two fragments, a soluble amino terminal fragment consisting cessentially of the extracellular domain, and a membrane bound fragment consisting of the transmembrane domain and the intracellular domain. The soluble fragment is able to bind to Notch. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention relates to the delta cleavage peptides (the active fragment), and to methods for detecting and measuring delta activation. Delta cleavage peptides, and chimeric proteins are useful for modulating the activity of Notch, delta or kuz or at least one of the signalling pathways in a cell or organism, expressing Notch. By contacting a cell with kuz protein or

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           EHYYGEGCSVFCRPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP
                                                                                               VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA
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                                         GECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN
                                                     GECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN
                                                                                  GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG
                                                                                                                                                                                                                                                                                                    KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                                                                                                                                                                                                                                                KRDTKCQPQGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVI
                                                                                                                            KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC
                                                                                                                                                                                                                 PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                           ATEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; delta-1 amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as leukaemia and malignant tumours, and improvement of blood formation, e.g. after immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide(s) encoded by human genes delta-1 and serrate-1 - suppress proliferation and differentiation of undifferentiated human blood cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF
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                                                                                                                                                                   Proliferation, differentiation, suppression, human, delta-1, serra
blood cell; neuron, leukaemia, malignant tumour; immunosuppression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 723;
                                                                                                                                                                                                                                                          22. 723
/label= Differentiation_suppression_protein
                                                                                                                                               Proliferation and differentiation suppression polypeptide.
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87.0%; Pred. No. 3.8e-205;
iive 46; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 77-82; 114pp; Japanese
                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                AAW18353 standard; protein; 723
                                                                                                                                                                                                                              1. .21
/label= Signal
22. .722
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95JP-00311811.
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                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 630, Conserv
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30-NOV-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                           Sakano S,
                          721
                                                                                                      AAW18353;
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Sakano S;
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          AAW94498
                            AAW94498;
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                                                                                                                                       Peptide
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                                                                                                                                                                                                                                                                                        EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKP 239
                                                                                                                                                                                                                                                                                                           240
                                                                                                                                                                                                                                                                                                                             GECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN 299
                                                                                                                                                                                                                                                                                                                                        GECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN 300
                                                                                                                                                                                                                                                                                                                                                                 GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359
                                                                                                                                                                                                                                                                                                                                                                           419
                                                                                                                                                                                                                                                                                                                                                                                                              361 KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                        479
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                                                               This sequence represents the human delta-1 protein, which is a ligand of the human notch protein. The protein or fragments, especially AAW75493-W75495, can be used as a drug to control vascular cells. The sequences were isolated and the truncated fragments were generated using the primers AAX16818-X16831
                                                                                                                                                                                              9
                 Vascular cell controlling agent comprises polypeptide - which is human notch ligand and is used as drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGPFPWVAVCAGVILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETWNLANCQRE
                                                                                                                                                                                        RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF
                                                                                                                                                                                                                                 61 RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF
                                                                                                                                                                                                                                                              660 KRDTKCQPQGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVI
                                                                                                                                                                                                                                                                                                                                                                                                     KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC
                                                                                                                                                                                                                                                                                                                                                                                                                                        VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI
                                                                                                                                                                             MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSG-PPCACRTFF
                                                                                                                                                           Gaps
                                                                                                                                                           3;
                                                                                                                                         Length 723;
                                                                                                                                                          45; Indels
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                                                                                                                                        ; Score 3659.5; DB 2; Pred. No. 3.8e-205; 46; Mismatches 45;
                                              21pp; Japanese.
                                                                                                                                         88.8%;
                                                                                                                                                 Best Local Similarity 87.0 Matches 630; Conservative
                                               Disclosure; Page 16-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATEV 722
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 N-PSDB; AAX16817.
                                                                                                                      Sequence 723 AA;
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RESULT 7

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The present invention describes full length and shortened human delta-2 proteins. Human delta-2 is a differentiation inhibitor which inhibits the differentiation of undifferentiated cells (other than brain or muscle cells), such as blood cells, and enhances the proliferation of undifferentiated blood cells. Products of human delta-2 may be used for the treatment of diseases such as leukaemia and malignant tumours. They may also be used in the culture of human cells in vitro, e.g. for production of supplies of undifferentiated blood cells. The present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                     Human, delta-1; delta-2; differentiation inhibitor; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence represents human delta-1, from an example of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide inhibiting the differentiation of undifferentiated blood for treatment of cancer and other disorders and the culture of hu cells in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
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87.0%; Pred. No. 3.8e-205;
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723
                                                                                                                                                                                                                                                                                                                                            22. .723
/label= Delta-1
                                                                                                                                                                                                                                                                                                    l. .21
/label= signal
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standard; protein;
                                                                                                                                                                                             leukaemia; malignant tumour
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                                                                                                                               Human delta-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-070120/06.
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                                                                                                                                                                                                                                                                                                                                                               169. 373
note= "Casein kinase II phosphorylation site"
178. 384
                               "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                        /note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660. .664
/note= "cAMP and cGMP dependent protein kinase
phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Casein kinase II phosphorylation site"
                                                                        /note= "Tyrosine kinase phosphorylation site"
262. .268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Casein kinase II phosphorylation site"
           "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                 'note= "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                             'note= "Asn and Asp hydroxylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Asn and Asp hydroxylation site"
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7 Jabel - Asn and Asp hydroxylation site

47. 47.9

7 Jabel - EGF-like_domain
                                                                                                                                                                                                                                    328. .334
/note= "N-myristoylation domain"
                                                                                                                                                                                                                                                        340. 346
/note= "N-myristoylation site"
                                                                                                                                                           /note= "N-myristoylation site"
                                                                                              "N-myristoylation site"
                                                                                                                                   /note= "N-myristoylation site"
282. .288
                                                                                                                                                                                                      site"
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/note= "N-glycosylation site"
183. .487
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/label= Transmembrane_domain
                                                                                                                                                                     301. .307 /
/note= "N-myristoylation
                                                                                                                                                                                                    /note= "N-myristoylation
314. .326
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                                                                                                                                                                                                                                                                                                                                                                                                          387. .393 /note= "N-myristoylation
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                                243. 255
/label= EGF-like_domain
252. 261
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/label= EGF-like_domain
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/label= EGF-like_domain
420. .432
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           /note= "Ty
203. .207
/note= "Ca
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/label= EG
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 GECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN 300
                                                               KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 718
                                                                                                                                                                                                                                                                                                                         GECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN 299
                                                   GATCTN/TGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359
                                                                                           KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC 419
                                                                                                                                     VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479
                                                                                                                                                                                PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ 539
                                                                                                                                                                                                                        GGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPBPCGGETETMNNLANCQRE 599
                                                                                                                                                                                                                                                                    KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
                                                                                                                                                                                                                                                                               Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131. .135
/note= "Casein kinase II phosphorylation site"
154. .158
/note= "Casein kinase II phosphorylation"
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'note= "Casein kinase II phosphorylation site"
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/label= Signal_peptide
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99. .105
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/note= "1
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                                   421 VDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSA
                                                                                                    PVSRCEHAPCHNGATCHERGHRYVCECARGYGGPNCQFLLPELPPGPAVVDLTEK-LEGQ
               VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA
                                                                                PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ
                                                                                                                                                  GGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQRE
                                                                                                                                                                     KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                                                                                                                                                                                                                       KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI
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99US-012361BP
99US-0123775P
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12-MAR-1999;
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12-APR-1999;
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04-MAY-1999;
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02-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359
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                                                                                                                                                                                                                                                                                                                                                                            Wood WI;
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                                                                                                                                                                     /note= "Casein kinase II phosphorylation site"
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"Casein kinase II phosphorylation site"
                                 "Casein kinase II phosphorylation site"
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88.8%; Score 3659.5; DB 3; Length
Best Local Similarity 87.0%; Pred. No. 3.8e-205;
Matches 630; Conservative 46; Mismatches 45; Indels
                                                                                                                  695. .701
/note= "N-myristoylation site"
698. .702
                                                                                                    "N-myristoylation site"
                                                                    "N-myristoylation site'
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/note= "N
        Goddard A,
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     note=
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N-PSDB; AAZ93703.
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61 RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTF 120
                                                                            121 SLIIEALHTOSPDDLATENPERLISRLATORHLTVGEEWSODLHSSGRTDLKYSYRFVCD
                                                                                                                                                                   181 EHYYGEGCSVPCRPRDDAFGHFTGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and disgnosing immune related disorders are useful for treating and disgnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Siogran's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune of diseases and transplantation associated diseases including graft rejection and graft-versus-host-disease. Ancessis the lung, and transplantation associated diseases including craft rejection and graft-versus-host-disease. Ancessis the sequences and Mybridisation probes used in the isolation of human PRO sequences. AACSSS79 to AACSSS78 represent PRO primers and Mybridisation probes used in the isolation of exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Pan J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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                     99WO-US020594
99WO-US021090
99WO-US021547.
99WO-US021889
99WO-US02814
99WO-US02814
99WO-US028818
99WO-US028818
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99WO-US028565.
99WO-US030095.
99WO-US030999.
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2000WO-US004342
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Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
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01-SEP-1999

08-SEP-1999

15-SEP-1999

15-SEP-1999

15-SEP-1999

16-OCT 1999

29-OCT 1999

20-NOV-1999

30-NOV-1999

01-DEC-1999

01-DEC-1999

02-DEC-1999

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02-DEC-1999

03-DEC-1999

04-DEC-1999

06-DEC-1999

06-DE
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11-FEB-2000;
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Human, PRÖ, promotion, inhibition, angiogenesis, cardiovascularisation, diagnosis, trauma, wound, cancer, atherosclerosis, cardiac hypertrophy, angiogenic, proliferative, cardiant, cardiovascular, antiatherosclerotic, cytostatic, gene therapy, vaccine.
                                                                   Human PRO172 protein sequence SEQ ID NO:4.
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AAB24388 standard; protein; 723
                                                                                                                                                                                                                                             98WO-US025108.
98US-0112850P.
99US-0115554P.
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                                            07-NOV-2000 (first entry)
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16-DEC-1998;
12-JAN-1999;
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RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF 119

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1 MGRRSALALAVVSALLCOVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSG-PPCACRTFF

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3; Сарв

45; Indels

, Pred. No. 3.8e-205, 46; Mismatches 45;

Conservative

Similarity

Best Local Simi Matches 630;

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VDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSA
                                                                                                                                                                   PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ
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                                              KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC
                                                                                                         VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA
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/note= "N-myristoylation
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/label= Signal peptide
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/note= "Ca:
176. .185
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/note= ":
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                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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Klein RD,
Wood WI;
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87.0%; Pred. No. 3.8e-205;
ive 46; Mismatches 45;
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, Gurney AL,
Williams PM,
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 99WO-US005028.
99US-013145FP
99US-01314287P
99WO-US012523
99WO-US012523
99US-0141037P
99US-014568P
99US-014568P
99WO-US020111.
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99WO-US021547.
99WO-US023089.
99US-0162506P.
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Goddard A, Godowski PJ,
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N-PSDB; AAA77512.
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 08-MAR-1999;
12-MAR-1999;
28-APR-1999;
02-JUN-1999;
23-JUN-1999;
20-JUL-1999;
01-SEP-1999;
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note= "EGF-like domain cysteine pattern signatu"
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74. .286
label= EGF-like domain cysteine pattern signatu
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//note= "N-myristoylation site"
391. 403
/label= EGF-like domain cysteine pattern signatu
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|abel= EGF-like domain cysteine pattern signatu
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phosphorylation site"
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|abel= Prokaryotic membrane lipoprotein lipid
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note= "Casein kinase II phosphorylation site"
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78. .384
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note= "Casein kinase II phosphorylation site"
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note= "Casein kinase II phosphorylation site"
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                      52. .261
note= "Tyrosine kinase phosphorylation site"
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/note= "Casein kinase phosphorylation site"
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note= "Casein kinase II phosphorylation
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|label= EGF-like domain cysteine
328. .334
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note= "Abx hydroxylation site"
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note= "Asx hydroxylation site"
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note= "Asx hydroxylation site"
                                                                       781. .287
Thote= "N-myristoylation site"
82. .288
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hote= "N-myristoylation site"
110 .316 myristoylation site"
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40. 346
note= "N-myristoylation site"
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/note= "N-myristoylation site"
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/note= "N-glycosylation site"
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label= Transmembrane
                                          . 268
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Isolated PRO211, PRO228, PRO518, PRO172 or PRO182 polypeptides or their agonists (preferably anti-PRO agonist antibody or a small molecule mimicking the biological activity of PRO polypeptide) are useful in vitro or inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic sgrowth and for treating cancer including breast, ovarian, renal, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, gilal, astrocytal, blastoccelic disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO monitoring biological activity mediated by the polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119
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             /note= "N-myristoylation site"
695. .701
/note= "N-myristoylation site"
690. .702
/note= "Casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                       Napier MA,
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99US-0131445P.
99US-0144758P.
99US-0145698P.
99WO-US020594.
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N-PSDB; AAA54105.
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Modified-site
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08-SEP-1999;
15-SEP-1999;
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241 GECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKN 300
                                                301 GATCTNTGQGSYTCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYG 360
                                                                                               361 KICELSAMTCADGPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKC 420
                                                                                                                                  VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA 479
                                                                                                                                              VDLGDAYLCRCQAGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSA 480
                                                                                                                                                                                  PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPWVVDLSERHMESQ 539
                                                                                                                                                                                               GGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQRE 599
                                                                                                                                                                                                                                              KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS 659
                                                                                                                                                                                                                                                                                            660 KRDTKCQPQGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYGSVYVISEEKDECVI 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostete; cervical; tumour necrosis factor-alpha; TNF-alpha; cattilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.
                                                                                  360 KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC
                                   GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PRO172 polypeptide sequence.
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99WO-US028551.
99WO-US028564.
99WO-US028565.
99WO-US030095.
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99WO-US031243.
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2000WO-US000219.
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02-DEC-1999;
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09-DEC-1999;
16-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
30-DEC-1999;
31-DEC-1999;
05-JAN-2000;
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ANUL2172-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactrive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of protecoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the proliferation of endothelial cells or of T-lymphocytes, the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor villa. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymclectides encoding PRO polypeptides can be used to generate PRO antisecence of the probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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L, Sherwood S;
od WI, Zhang Z;
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Gerritsen ME, Goddard A, Godowski
Smith V, Stewart TA, Tumas D, Wat
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2000WO-US014042.
2000WO-US014941.
2000WO-US015264.
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2000US-0187202P.
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2000WO-US006884.
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Best Local Similarity 87.0
Matches 630; Conservative
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                                                                                                     24 - FEB - 2000;
24 - FEB - 2000;
20 - MAR - 2000;
03 - MAR - 2000;
01 - MAR - 2000;
15 - MAR - 2000;
20 - MAR - 2000;
21 - MAR - 2000;
30 - MAR - 2000;
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02-JUN-2000;
05-JUN-2000;
28-JUL-2000;
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22-MAY-2000;
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3; Gaps

1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSG-PPCACRTFF

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14-SEP-2000

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KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC 419
                                                                            GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359
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MGSRCALALAVLSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFF
                                                                                                                                                                                RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF
                                                                                                                                                      SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD
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The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AABS3064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins compraining a PRO protein, expression of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO carpitals or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO source of a protein, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO mucleic acids, PRO protein, or an agonist or antagonist thereof. PRO agonist cands who proteins, antibodies against PRO proteins, PRO andiched and proteins, PRO cardiovascular or antagonist thereof. PRO agonist cands applied to a magonist can antagonist the protein and agonist cands and proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular, endochelial or anajogenic disorders, such as atheroscients, endochelial or anajogenic disorders, such as atherosciencesis, osteoporosis, myocardial infarction, hypertension, diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis, endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridiation probes to screen libraries to isolate cobns with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or anglogenic disorders, such as atherosclerosis, wounds or cancer.
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Mark MR, Marsters SA;
1, Wood WI;
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Jurney AL, Hillan KJ, Kuo SS, Ma
i RM, Watanabe CK, Williams PM,
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99US-0141037P.
99US-0144758P.
99US-0145698P.
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Godowski PJ, Gurney
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Query Match 88.8*; Score 3659.5; DB 4 Best Local Similarity 87.0*; Pred. No. 3.8e-205; Matches 630; Conservative 46; Mismatches 45;

WO200053753-A2

4; Length 723; Indels

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18-FEB-2000;
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10-SEP-1998;
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                  Homo sapiens
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                  RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF
                                                                                                                                          SLITEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD
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The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 275 nucleotide sequences, and which encodes a corresponding codypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a CR propolypeptide, modulate a biological activity of a cell, stimulate the telease of tumour necrosis factor (TNF)-alpha from human blood, modulate the proliferation or differentiation of cells, stimulate cor inhibit the proliferation or differentiation of cells, stimulate cor inhibit constituents are stimulate the release of proteoglycans, stimulate the release of cytokine stimulate the release of proteoglycans, stimulate the release of cytokine constituents are sequenced to tumour in a mammal. The nucleic coff and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atheroscletosis, cardiac injury, infertility, brith defects, premature aging, acquired immunodeficiency syndrome condisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as harmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-JUN-2001; 2001WS-00872035.
01-JUN-2001; 2001WS-US017800.
05-JUN-2001; 2001WS-00874503.
14-JUN-2001; 2001US-00886342.
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2001WO-US006666.
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19-DEC-2001; 2001US-00028072
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ME, Goddard A,
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anti-PRO antibody, diagnostic assay, gene expression, diabetes,
                                                Length 723;
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9
                                                Query Match

88.8%; Score 3659.5; DB 6
Best Local Similarity 87.0%; Pred. No. 3.8e-205,
Matches 630; Conservative 46; Mismatches 45;
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transmembrane PRO polypeptide
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bone disorder; cartilage disorder; rheumatoid arthritis; obesity; sports injury; osteoarthritis; hyper-insulinaemia; hpo-insulinaemia; hearing loss; coagulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic.
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9705-0056974P

9705-0059115P

9705-0059113P

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29-0CT-1997;
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24-SEP-1997
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New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or heart attack.
                                                                                                                                                                                                                                                                                                                                                      Deforge L, Desnoyers L, Filvaroff E, G
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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99WO-US020944
99WO-US0211690
99WO-US023089
99WO-US028214
99WO-US028313
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2000WO-US000277.
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               98WO-US022992.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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30-DEC-1999;
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29-NOV-19
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Gao

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are secreted and transmembrane proteins. The PRO useful in the treatment of diabetes, bone and/or cartilage disorders (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity, hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, issues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABUS0870-ABUS1144 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent sequata.uspto.gov/psipsDDEntry.html

Sequence 723 AA;

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  88.8%; Score 3659.5; DB 6; Length 723; 87.0%; Pred. No. 3.8e-205; ive 46; Mismatches 45; Indels 3;
Query Match
Best Local Similarity 87.0
Matches 630; Conservative
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-908-322-12
US-08-872-855-4
US-08-872-855-4
US-09-168-740A-9
US-09-168-740A-9
US-09-168-740A-4
US-09-168-740A-4
US-09-908-322-2
US-09-908-322-2
US-09-908-322-5
US-09-908-322-5
US-09-908-322-5
US-09-908-322-13
US-08-872-855-9
US-08-872-855-9
US-08-872-855-9
US-08-91-392-13
US-08-872-855-9
US-08-872-855-9
US-08-872-855-9
US-08-872-855-2
US-09-423-753-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match
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Perfect score:
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Sequence 6, A
Sequence 2, A
Sequence 2, A
Sequence 6, A
Sequence 11,
Sequence 6, A
Sequence 6, A
Sequence 10,
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                                   US-08-465-500-6
US-08-346-126-6
US-08-346-126-6
US-08-3512-384-2
US-08-931-32-6
US-09-901-32-6
US-09-901-32-6
US-09-917-25-6
US-09-917-25-85
US-09-917-25-85
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US-09-917-25-85
US-09-917-25-85
US-09-9195-52-41
US-08-611-729A-10
US-08-611-729A-10
US-08-611-729A-10
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US-08-611-729A-10
US-08-812-046-5
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STATE: NY
COUNTRY: USA
ZIP: 10036/271
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: FastSEQ Version 2.0
SOFTWARE: 22-DEC-1997
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: AALIST, Addiane M
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMAT
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
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100.0%; Pred. No. 1.7e-301
Live 0; Mismatches 0;
                                                                                                                         FILING DATE: 17-U1-20(1)
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 1326-123
TELECOMMUNICATION INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                          TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 722 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: <Unknown>
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Best Local Similarity 100.
Matches 722; Conservative
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                          MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR
                                                                                             61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS
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Patent No. 6783956
GENERAL INFORMATION:
GENERAL INFORMATION:
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
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the Americas
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ADDRESSES: Pennie & Edmonds LL
STREET: 1155 Avenue of the Ame
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
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INVENTION: NUCLEOTIDE /
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                                                                        239 ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG
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APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 11-JUN 1997
CLASSIFICATION: 514
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ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-(TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
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STATE: MA
COUNTRY: USA
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719 EV 720
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               DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK
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Fatent No. 6121045
GENERAL INPORMATION:
APPLICANT: McGaring, David
ITILE OF INVENTION: THERAPEUTIC USES THEREFOR
INVERSE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: U1-JUN-1997
CLASSIFICATION: 514
ATTOMNEY/AGENT INPORMATION:
NAME: ATTOHOL BET BE:
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: 35,430
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 617-832-1000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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Best Local Similarity 97.0
Matches 700; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: MA
COUNTRY: USA
TO: 02109-2170
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                                                                                                DB 3; Length 713;
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                                                                                         udery Match
Best Local Similarity 93.4%; Pred. No. 2e-280;
Matches 674; Conservative 11; Μίεπατκήρε <sup>γ</sup>
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
TYPE: amino acid
                              TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-09-068-740A-9
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Sequence 9, Application US/09068740A Patent No. 6337387 GENERAL INFORMATION:

APPLICANT: SAKANO, SELJI APPLICANT: ITOH, AKIRA

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TITLE OF INVENTION: DIFFERENTIATION-SUPPRESS
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/9/068,740A
CURRENT FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: UP 7-29611
PRIOR RILING DATE: 1995-11-17
PRIOR APPLICATION NUMBER: UP 7-311811
PRIOR FILING DATE: 1995-11-30
PRIOR FILING DATE: 1995-11-15
PRIOR FILING DATE: 1996-11-15
PRIOR FILING DATE: 1996-11-15
SRO ID NOS: 48
SOFTWARE: PALENTIN Ver. 2.1
SRO ID NO 9
LEAST OF THE STORY OF TH
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; ORGANISM: Homo sapiens
US-09-068-740A-9
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630; Conserv
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Best Local S:
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Sequence 346, Application US/10140002
Patent No. 6725730
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                           Desnoyers, Luc
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                DeForge, Laura
                                                                                                                                                                                                                                       Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo Sapien
US-10-140-002-346
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Best Local Similarity
Matches 630; Conserv
                          719 ATEV 722
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                     88.8%; Score 3659.5; DB 4; Length
87.0%; Pred. No. 8e-267;
ive 46; Mismatches 45; Indels
                                                                                             INHIBITOR
                                 Sequence 27, Application US/09423753
Patent No. 6664098
GENERAL INFORMATION:
PAPLICANT: SARANO, SELJI
TITLE OF INVENTION: NOVEL DIFFERENTIATION INH
FILE REFERENCE: KP-8693
CURRENT APPLICATION NUMBER: US/09/423,753
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: US/09/423,753
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-13
PRIOR FILING DATE: 1997-05-14
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 87.0
Matches 630; Conservative
                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-753-27
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APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT APPLICATION NUMBER: US/10/140,002
PRIOR APPLICATION TEMOVED - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
550 ID NOS: 550
550 ID NOS: 550
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87.0%; Pred. No. 8e-267;
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| APPLICANT: SAKANO, SELJI
| APPLICANT: ITOH, AKIRA
| TITLE OF INVENTION: DIPFERENTIATION-SUPPRESSIVE POLYPEPTIDE
| FILE REFERENCE: KP-8447 |
| CURRENT APPLICATION NUMBER: US/09/068,740A |
| FILE REPERSONCE: 1996-6118 |
| PRIOR APPLICATION NUMBER: UP 7-299611 |
| PRIOR PILING DATE: 1995-11-17 |
| PRIOR PILING DATE: 1995-11-17 |
| PRIOR PILING DATE: 1995-11-16 |
| PRIOR PILING DATE: 1995-11-16 |
| PRIOR PILING DATE: 1995-11-15 |
| NUMBER OF SEQ ID NOS: 48 |
| SEQ ID NOS: 40 |
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87.1%; Pred. No. 3.2e-260;
ive 45; Mismatches 43;
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Best Local Similarity 87.1<sup>3</sup>
Matches 612, Conservative
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ORGANISM: Homo sapiens
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                                            KDVSVSIIGATOIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
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                            VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA
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86.5%; Pred. No. 1e-264;
Micmatches 49;
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TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS ANI
FILE REFERENCE: PPO-1602.02 / 200100.498
CURRENT APPLICATION NUMBER: US/09/641,612
CURRENT FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 723
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-641-612-6
; Sequence 6, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
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Best Local Similarity 86.5
Matches 626; Conservative
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ORGANISM: Homo sapiens
US-09-641-612-6
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                                                                                                                                                                                                                                                                     CACRIFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGA-GIDPAFSNPIRFPF
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                                                                                                                                                                                                 1 MGRRSALALAVVSALL--CQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGP----P
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                                                                                                                                                                 12;
                                                                                                                         Length 728;
                                                                                                                                                             Indels
                                                                                                                           DB 3;
                                                                                                                                          ; Pred. No. 6.5e-245; 73; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Herrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                           81.7%; Score 3368; 78.5%; Pred. No. 6.5
LENGTH: 728 amino acids
                                                                                                                                                               Conservative
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EKDECIIATEV 728
                                                   TOPOLOGY: unknown
MOLECULE TYPE: protein
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                  TYPE: amino acid STRANDEDNESS:
                                                                                                                                            Best Local Similarity
Matches 574; Conserv
; LENGTH: ; ; TYPE: ami; ; STRANDEDNE; ; TOPOLOGY: ; MOLECULE TYPE US-08-981-392-2
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US-09-908-322-2
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               GCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTNTGQGSYTCSCRPGYT 320
                                                                                                          SDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVDLGNSYLCRCQAGFSGRYCE 440
                                                                                                                                                                                DNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHNGATCHERGH 480
                                                                                                                                                                                                                                                                                                                              241 GCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSYTCSCRPGYT 300
                                                                                     GANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGKVCELSAMTCADGPCFNGGRC 380
                                                                                                                                                                                                                                     DNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGATCHQRGQ 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          FHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSKRDTKCOSO-SLOEKRRSPOH 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: ISh-Horowicz, David

APPLICANT: Henrique, Domingos Manuel Pinto

APPLICANT: Hewis, Julian Hart

APPLICANT: Lewis, Julian Hart

APPLICANT: Artavanis-Teakonas, Spyridon

APPLICANT: Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES

TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIATEV 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPAX: 212-869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FRAELSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08981392
Patent No. 6262025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
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NAME: Antler, Adriane M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-981-392-2
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                               472 YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL
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APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
CONTRY: WA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 81.5%; Score 3357.5; DB 3; Best Local Similarity 78.4%; Pred. No. 4e-244; Matches 574; Conservative 73; Mismatches 72;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08872855 Patent No. 6121045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ARIOLA, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA.
TELECHONE: 617-832-1000
TELEPHONE: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35,430
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amino acid
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EKDECIIATEV 728
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-872-855-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 GFTWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLK 179
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Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASISCO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION OFF: 08/981,392
ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                   nonds LLP
the Americas
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LENGTH: 728 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: «Unknown:
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-908-322-2
                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonde
STREET: 1155 Avenue of the A
CITY: New York
                                                                                                                                                                             STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
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Matches 574; Conservative
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원 ઠે ద ò a ò g ઠે 셤 ò 임 8

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361 YGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCEKKIDYCSSNPCANGA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDT 657
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                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version
                                                                                                                                                                                                                                                                                                                                                                76.9%;
                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.9% Matches 534; Conservative
                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                            unknown
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TOPOLOGY: ur
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                                            CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF 119
                                                                                                        TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS 419
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                                                                                        GFTWPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLR 171
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MGGRFLLTLALLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGG-GPGGAGOOO
                            CACRTFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGA-GIDPAFSNPIRFPF
                                                                                                                                                  172 YSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDD
                                                                                                                                                                   180 YSYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDE
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Sequence 5, Application US/08981392
Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Inh-Horowicz, David
APPLICANT: Inh-Horowicz, David
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASE
NUMBER OF SEQUENCES:
ADDRESSEE: Pennie & Edmonds III
STREET: 1155 Average
CTTV.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-08-981-392-5
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                                                                                                                                              KPGECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC
                                                                                                                                                                                                                                                             RNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       658 HSKRDTKCQS------QSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVL
                                                                                                                                                                                                                                                                                             301 ENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDANPCKNGGSCSDLENSYTCSCPPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 SQGGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, Daving, Dav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PARM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
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ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/08872855 ; Patent No. 6121045
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709 SDEKDECIIATEV 721
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STATE: MA
COUNTRY: U
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||:| ||||||||||||||---RRRPDSAYSTSKDTKYQSVYVI 708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPP---CACRT
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72.9%; Pred. No. 7.5e-230;
tive 89; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFFWARE: Fast SEQ. Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09908322
Patent No. 6783956
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                      710 SAEKDECVIATEV 722
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709 SDEKDECIIATEV 721
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Best Local Similarity 72.9
Matches 534; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                     RESULT 14
US-09-908-322-5
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                                                                                                                                                                                                                                                                                    CDEYYYGEGCSDYCRPRDDAFGHFSCGEKGENLCNPGWKGLYCTEPICLPGCDEHHGYCD 240
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                                                                                                                                                             SMPITKCEHNPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPEEK--PVVVDLTEKYTE
                                                                                                                                                  MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPP---CACRT
                                                                                                                                                                                                                                                                        CDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEXMCDPGWKGQYCTDFICLPGCDDQHGYCD
                                                                                                                                Gaps
                                                                                                                               23;
                                                                                                          Query Match

76.7%; Score 3161.5; DB 3; Length 721;
Best Local Similarity 72.7%; Pred. No. 2.1e-229;
Matches 533; Conservative 89; Mismatches 88; Indels 23;
      TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: 1.ENGTH: 721 amino acids TYPE: amino acid STRANDEDNESS: 1.TOPOLOGY: linear 1.TOPOLOGY: linear 1.TOPOLOGY: linear 1.TYPE: protein US-08-872-855-7
617-832-1000
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| SDEKDECIIATEV 721
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Search completed: November 29, 2004, 13:28:04 Job time : 23.2231 secs

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November 29, 2004, 13:26:20 ; Search time 72.7322 Seconds (without alignments) 3520.994 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                         Copyright
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 12, Appl	Sequence 12, Appl	Sequence 107, App	Sequence 4, Appli	Sequence 4, Appli	Sequence 108, App	Sequence 5, Appli	Sequence 21, Appl	Sequence 9, Appli	Sequence 346, App	Sequence 346, App	346,	Sequence 346, App
SUMMARIES	. OI	US-09-908-322-12	US-09-783-931-12	US-10-042-865-107	US-10-731-741-4	US-10-417-719-4	US-10-042-865-108	US-10-417-719-5	US-09-828-366-21	US-09-995-593A-9	US-10-028-072-346	US-10-140-808-346	US-10-121-049-346	US-10-123-904-346
	DB	0	70	15	16	14	15	14	σ	σ	14	14	14	14
	Query Match Length DB ID	722	722	722	722	720	714	713	723	723	723	723	723	723
عد	Query	100.0	100.0	97.1	97.1	96.4	93.4	93.2	88.8	88.8	88.8	88.8	88.8	88.8
	Score	4121	4121	4003	4003	3971	3848	3840.5	3659.5	3659.5	3659.5	3659.5	3659.5	3659.5
	Result No.	-	8	е	4	S	9	7	80	6	10	11	12	13

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-10-140-470-34 -10-175-746-34 -10-176-918-34	US-10-137-845-346 US-10-140-431-346 US-10-142-431-346 US-10-140-002-346 US-10-140-002-346 US-10-142-419-346 US-10-142-419-346 US-10-142-423-346 US-10-141-050-346 US-10-141-050-346 US-10-123-261-346 US-10-123-261-346 US-10-123-292-346 US-10-123-292-346 US-10-124-822-346 US-10-124-822-346 US-10-124-822-346 US-10-124-822-346 US-10-124-822-346 US-10-124-824-346 US-10-124-824-346 US-10-127-825A-346 US-10-127-825A-346 US-10-127-825A-346	ALIGNMENTS
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LIGNMENT

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US-0908-322-12

US-0908-322-12

Sequence 12, Application US/09908322

Patent No. US20020107194A1

GENERAL INFORMATION:

Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Teakonas, Spyridon
Gray, Grace

TITLE OF INVENTION: WUCLEOTIDE AND PROTEIN SEQUENCES OF

VERTEBRATE DELTA GENE AND METHODS BASED THEREON
WUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonda LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: N

COUNTRY: USA
COUNTRY: USA
CONPUTER: READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: LOSS
SOFTWARE: FastSEQ Version 2.0

CURRENT SAPLICATION DATA:

APPLICATION NUMBER: US/09/908,322

FILING DATE: 17-Jul-2001
CLASSIFICATION NUMBER: US/09/908,322

FILING DATE: 12-Jul-2001
CLASSIFICATION NUMBER: US/09/908,322

FILING DATE: 12-DEC-1997

ATTORNEY/AGENT INFORMATION:
NUMBER: MSECISTALION:
NUMBER: MSECISTALION:
NUMBER: MSECISTALION:
NUMBER: MSECISTALION NUMBER: 18 972

REFERENCE/DOCKET NUMBER: 18 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
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                                                                                                                                                                                                                                                                                                        VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG
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                                                                                                                                                                                            Query Match 100.0%; Score 4121; DB 9; Length 722; Best Local Similarity 100.0%; Pred. No. 4.3e-272; Matches 722; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                           ) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-908-322-12
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-869-8060
TELEFAX: 212-869-8064
TELEX: 66141 PENNIE
INFORMATION FOR SEG ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acid
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: unknown>
TOPOLOGY: unknown>
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RESULT 2 US-09-783-931-12

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100.0%; Pred. No. 4.3e-272;
iive 0; Mismatches 0;
                                                                                      Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COMPACIDE
COMPUTER: IBM COMPACIDE
SPERATING SYSTEM: DOS
SOFTWARE: FARLSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 08/981,392
ATTORNEY/AGENT INFORMATION:
NAME: AND TO THE APPLICATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
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STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
WOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO
AND FRAGMENTS
Sequence 12, Application US/09783931
Publication No. US/030073620A1
GENERAL INFORMATION:
APPLICANT: I6h-Horowicz, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity 100.
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                                                                                                                                                     VSRCEHAPCHNGATCHQRGQRYMCECAQGGGGPNCQFLLPEPPPGPMVVDLSERHMESQG
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                                       VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV
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APPLICANT: Caennan, Stace J
APPLICANT: Shenoy, Sureeh G
APPLICANT: Shongy, Meren G
APPLICANT: Spytek, Kimberly
APPLICANT: Shongy, Meren
APPLICANT: Burgess, Catherine E
APPLICANT: Patturajan, Meera
APPLICANT: Teherney, Velizar T
APPLICANT: Teherney, Velizar T
APPLICANT: Teherney, Velizar T
APPLICANT: Miler, Charles E
APPLICANT: Miler, Charles E
APPLICANT: Miler, Charles E
APPLICANT: Geraece L
APPLICANT: Geraece L
APPLICANT: Alsobrook II, John P
APPLICANT: Belnege, Malk E
APPLICANT: MacDougall, John P
APPLICANT: MacDougall, John
APPLICANT: Malenberg, Mark E
APPLICANT: Milet, Isabelle
APPLICANT: Milet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Stone, David
TITLE OF INVENTION: Perceins, Polynucleotides Encoding Them
TITLE OF INVENTION: Verceins, Polynucleotides
FILE REFERENCE: 21402-537
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CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
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, Sequence 107, Application US/10042865
, Publication No. US20040029216A1
, GENERAL INFORMATION:
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
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                                                                                                                                                                                                                                                                                                                                      Query Match 97.1%; Score 4003; DB 15; Best Local Similarity 97.2%; Pred. No. 4.6e-264; Matches 702; Conservative 4; Mismatches 16;
PRIOR APPLICATION NUMBER: 60/260,831
PRIOR FILING DATE: 2001-01-0
PRIOR APPLICATION NUMBER: 60/272,338
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR PILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PALENTIN Vex: 2.1
SEQ ID NO 107
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DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 478
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APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean
APPLICANT: McCarthy, Sean
TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 08/812,855
PRIOR FILING DATE: 1997-06-11
PRIOR PILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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llarity 97.0%; Pred. No. 6.9e-262;
Conservative 4; Mismatches 16;
                                                                                                                                             Sequence 4, Application US/10417719
Publication No. US20030180784A1
GENERAL INFORMATION:
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US-10-417-719-4
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Best Local Similarity
Matches 700; Conserv
Z=2
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        Sequence 4, Application US/10731741

Sequence 4, Application US/10731741

Publication No. US20040171148A1

GENERAL INFORMATION:

APPLICANT: Schmitt, Thomas M.

APPLICANT: Schmitt, Thomas M.

APPLICANT: Schmitt, Thomas M.

TITLE OF INVENTION: Cell Preparations Comprising Cells of the T Cell

TITLE OF INVENTION: Lineage and Methods of Making and Using Them

FILE REFERENCE: 2223-171

CURRENT PILING DATE: 2003-12-10

PRIOR PILING DATE: 2003-12-10

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 722
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Pred. No. 4.6e-264;
4; Mismatches 16;
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Best Local Similarity 97.2%;
Matches 702; Conservative
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-10-731-741-4
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241 ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLPCWQDLNYCTHHKPCRNG 300
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                                                                                                                                61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRPPFGFTWPGTFS
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                                                                                      1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR
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     Length 714;
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Publication No. US20030180784A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarchy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
FILE REFERENCE: MBIO1997-002CP2M
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2000-05-09
PRIOR FILING DATE: 2000-05-09
PRIOR FILING DATE: 1997-06-11
   93.2%; Score 3848; DB 15; 93.2%; Pred. No. 1.6e-253;
               Pred. No. 1.6e-253
                                 13; Mismatches
                    Best Local Similarity 93.2%
Matches 673; Conservative
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EV 714
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                                                                   RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
                                                                                                                                    APPLICANT: Smithson, Glennda
APPLICANT: Sucher, Erik
APPLICANT: Stone, David
TITLE OF INVENTION: Proceins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 2140.2.53,
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-04-18
NUMBER: OF SEQ ID NOS: 264
SEQ ID NO 108
LENGTH: 714
                                                                                                                                                                                                                                                                                            Sequence 108, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Mera
Vernet, Corine A.M
Taylor, Sarah
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Miller, Charles E
Moldog, Radja
Boldog, Radja
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie
Edinger, Shlomit R
Rothenberg, Mark E
Blerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                             Li, Li
Zerhusen, Bryan D
Zesman, Stacie J
Shanoy, Suresh G
Spytek, Kimberly
Zhong, Mei
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; ORGANISM: Rattus norvegicus
US-10-042-865-108
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                                                                                                                           Gaps
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                                                                                                       14; Length 713;
                                                                                                     Query Match 93.2%; Score 3840.5; DB 1. Best Local Similarity 93.4%; Pred. No. 5.2e-253; Matches 674; Conservative 11; Mismatches 28;
                                                             TYPE: PRT
ORGANISM: Rattus No. US20030180784Alvegicus
PRIOR APPLICATION NUMBER: 08/832,633
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 713
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Sequence 21, Application US/09828366 Patent No. US200200137A1 GENERAL INFORMATION:
APPLICANT: Genencech, Inc.

RESULT 8 US-09-828-366-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF
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          APPLICANT:
APPLICANT:
Goddard, Audrey
APPLICANT:
Gurney, Austin L.
APPLICANT:
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APPLICANT:
APPLICANT:
Yuan, Jean
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE REFERENCE: P1694RICI
CURRENT FILING DATE: 2001-04-05
Prior filing data removed - refer to PALM or
NUMBER OF SEQ ID NOS: 29
SEQ ID NOS: 29
Ashkenazi, Avi
Goddard, Audrey
Gurney, Austin L.
Klein, Robert D.
Napier, Mary
Wood, William I.
Yuan, Jean
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.8
Best Local Similarity 87.0
Matches 630; Conservative
                                                                                                                                                                                                                                                                                                                           TYPE: PRT CORGANISM: Homo Sapien US-09-828-366-21
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540 GGPFPWVAVCAGVILVLMLLLGCAAVVVCVRLRLQKHRPPADPCRGETETMNNLANCQRE 599
                                                          KDVSVSIIGATOIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                                            660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/04911
PRIOR APPLICATION NUMBER: 60/05974
PRIOR APPLICATION NUMBER: 60/05974
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR PLICATION NUMBER: 60/059113
PRIOR PLICATION NUMBER: 60/059113
PRIOR PLICATION NUMBER: 60/059117
PRIOR FILING DATE: 1997-09-17
                                                                                                                                                                                                                                                                                                       ; Sequence 346, Application US/10028072; Publication No. US20030004311A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1997-09-24
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062285
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/059352
FILING DATE: 1997-09-19
APPLICATION NUMBER: 6/059588
FILING DATE: 1997-09-19
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PRIOR FILING DATE: 1997-09-18
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APPLICATION NUMBER: 60/062814
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APPLICATION NUMBER: 60/062816
FILING DATE: 1997-10-24
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Wood, William
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Filvaroff, Ellen
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TITLE OF INVENTION:
FILE REFERENCE:
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                                                                                           Sequence 9, Application US/0995593A

Patent No. US2020128197A1

GENERAL INFORMATION:
APPLICANT: SAKANO, SELJI
APPLICANT: STAKANO, SELJI
CURRENT APPLICATION NUMBER: US/09/995,593A
CURRENT FILING DATE: 1998-06-18
PRIOR PILING DATE: 1998-06-18
PRIOR PELING DATE: 1998-11-17
PRIOR PELING DATE: 1995-11-17
PRIOR PELING DATE: 1995-11-13
PRIOR PELING DATE: 1995-11-15
PRIOR SEQ ID NOS: 48

SOFTWARE: PATENTIN VUMBER: PCT/JP96/03356

NUMBER OF SEQ ID NOS: 48

SEG ID NO 99

SEG ID NO 99
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87.0%; Pred. No. 1.1e-240;
ive 46; Mismatches 45;
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Best Local Similarity 87.0
Matches 630; Conservative
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ATEV 723
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US-09-995-593A-9
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ORGANISM:
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R FILING DATE: 1998-06-23

R APPLICATION NUMBER: 60/090429

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R FILING DATE: 1998-06-24

R PILING DATE: 1998-06-24

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-06-26

R RILING DATE: 1998-06-26

R APPLICATION NUMBER: 60/090863

R FILING DATE: 1998-07-01 R FILING DATE: 1998-04-15

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R R FILING DATE: 1998-04-15

R APPLICATION NUMBER: 60/081818

R FILING DATE: 1998-04-24

R FILING DATE: 1998-04-24

R FILING DATE: 1998-04-28

R RILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/081545

R APPLICATION NUMBER: 60/081650

R APPLICATION NUMBER: 60/086519

R APPLICATION NUMBER: 60/0865149

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R APPLICATION NUMBER: 60/085149

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R APPLICATION NUMBER: 60/085139

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R FILING DATE: 1998-06-10

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R APPLICATION NUMBER: 60/08858

R FILING DATE: 1998-06-11

R APPLICATION NUMBER: 60/089532

R FILING DATE: 1998-06-17

R PILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089997

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/089997

R FILING DATE: 1998-06-17

R APPLICATION NUMBER: 60/08997

R FILING DATE: 1998-06-18

R APPLICATION NUMBER: 60/08997

R FILING DATE: 1998-06-19

R PILING DATE: 1998-06-19

R PILING DATE: 1998-06-19 R FILING DATE: 1998-05-22
R APPLICATION NUMBER: 60/087106
R FILING DATE: 1998-05-28
R PELICATION NUMBER: 60/088026
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088730 PRIOR APPLICATION NUMBER: 60/091519 PRIOR FILING DATE: 1998-07-02 PRIOR PAPLICATION NUMBER: 60/091982 PRIOR FILING DATE: 1998-07-07 REPRESENTATION OF THE PROPERTY OF THE PROPERTY

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Stewart, Timothy A.
                                                                                                                                                                                           Query Match
Best Local Similarity 87.0%
Matches 630; Conservative
                                                                                                                                                 TYPE: PRT

ORGANISM: Homo Sapien

US-10-140-808-346
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                                                                                                                 SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD 179
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                                                                                                                                                                                                                                                GATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359
                                                                                                                                                                                                                                                                                         KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC 419
                                                                                                                                                                                                                                                                                                                                                                              PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRDTKCOPOGSSGEEKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVI 719
                                                    9
                                                                                                                              SLIIBALHTDSPDDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCD
                                           1 MGSRCALALAVISALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPPCACRTFF
                                                                                     EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKP
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                                MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSG-PPCACRTFF
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            Gaps
           45; Indels
 87.0%; Pred. No. 1.1e-240;
ive 46; Mismatches 45;
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US-10-140-808-346
Sequence 346, Application US/10140808
Publication No. US20030017563A1
GENERAL INFORMATION:
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APPLICANT: Beresini, Maureen
APPLICANT: Beresini, Maureen
APPLICANT: Desnoyers, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Goo, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
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Filvaroff, Ellen
Gao, Wei, -Qiang
Gerritsen, Mary E.
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Best Local Similarity 97.0
Matches 630; Conservative
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                                                                                        NUCLEIC
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APPLICANT: Tumas, Daniel
APPLICANT: Watenabe, Colin K
APPLICANT: Watenabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P33330R1C182
CURRENT APPLICATION NUMBER: US/10/140,808
CURRENT FILING DATE: 2002-05-07
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length
                                                                                                                                                                                                                                                                                                                                                                                                                   45; Indels
                                                                                                                                                                                                                                                                                                                                                                         88.8%; Score 3659.5; DB 1487.0%; Pred. No. 1.1e-240;
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PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ
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Publication No. US20030022328A1
GENERAL INFORMATION:
APPLICANT: Baker.Kevin P.
APPLICANT: Beresini, Maureen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
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Best Local Similarity 87.0%,
Matches 630; Conservative
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; ORGANISM: Homo Sapien
US-10-123-904-346
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330RIC17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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                                                          Sequence 346, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION:
                                                                                                                                                    Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Stewart, Timothy A.
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Wood, William
                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Matches 630; Conservative
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APPLICANT:
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APPLICANT: Smith, Victoria
APPLICANT: Stewart Timochy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wacanabe, Colin K
APPLICANT: Anod, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123, 904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 3-46
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                                                                                                                                KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                                                                                      1 MGSRCALALAVLSALLCOVWSSGVPELKLOBFVNKKGLLGNRNCCRGGAGPPPCACRTFF
                                                    GGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPFPCGGETETMNNLANCQRE
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; Pred. No. 1.1e-240;
46; Mismatches 45; Indels 3:
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660 KRDTKCQSQ-SLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVI 718
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                                                                                               1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSG-PPCACRTFF
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                     88.8%; Score 3659.5; DB 14; Lenses 87.0%; Pred. No. 1.1e-240; Light Mismatches 45; Indels
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Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gezritgen, Mary E.
APPLICANT: Goodwaki, Paul J.
APPLICANT: Goddard, Audrey,
APPLICANT: Goddwaki, Paul J.
                                                                Conservative
                                                  Best Local Similarity
Matches 630; Conserv
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US-10-175-746-346
      US-10-140-470-346
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garitlean, Mary B.
APPLICANT: Garitlean, Mary B.
APPLICANT: Goddard, Austin L.
APPLICANT: Shewood, Steven
APPLICANT: Shewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Danis, Colin K.
APPLICANT: Tumas, Danis, Colin K.
APPLICANT: Wood, William
APPLICANT: Abendo, William
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Abond, William
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Abond, William
APPLICANT: MARNERE: USJ010/140, 470
CURRENT APPLICANION NUMBER: USJ02-05-06
CURRENT APPLICANION NUMBER: USJ02-05-06
CURRENT APPLICANION NUMBER: USJ02-05-06
                                                                                                          GATCTINTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG 359
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                                              GATCTNIGGGSYTCSCRPGYIGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 346, Application US/10140470 Publication No. US20030022331Al GENERAL INFORMATION: APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapien
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APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, william
APPLICANT: Wood, william
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C353
CURRENT APPLICATION NUMBER: US/10/175, 746
CURRENT APPLICATION TOWNER: US/10/175, 746
CURRENT APPLICATION TOWNER: US/20/206-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Best Local Similarity 87.0%; Pred. No. 1.1e-240;
Matches 630; Conservative 46; Mismatches 45; Indels
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K
                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-346
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Search completed: November 29, 2004, 13:42:00 Job time: 74.7322 secs
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ATEV 719

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
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sw model - protein search, using OM protein November 29, 2004, 13:16:29 ; Search time 18.0943 Seconds (without alignments) 3839.238 Million cell updates/sec Run on:

US-09-783-931-12

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

88

seq length: 0 seq length: 200000000 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ΩI	83	150719	JC7570	JC7569	S19087	A31246	800670	A56136	S16148	A35844	A46019	S18188	A40136	842612	A49175	A49128	A40043	T30201	T31070	S78549	A24420	845306	A35672	T09059	A48825	A48836	T25933	S53718	A56175
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	Score	4003	3368	1879.5	1828	1468.5	1463.5	1463.5	1312	1130	810	807.5	794.5	771	765.5	761	191	759	756	753	747	747	742	711	702.5	698	682	632	628	623
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A54785	806434	853716	A32901	B36665	A36665	T42218	E89753	JC7125	T22025	D89711	T30176	T42626	T13953	B49175	T08618
2 A54785	2 \$06434	2 \$53716	2 A32901	2 B36665	2 A36665	2 T42218	2 E89753	2 JC7125	2 T22025	2 D89711	2 T30176	2 T42626	2 T13953	2 B49175	2 T08618
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ALIGNMENTS

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DELTA-like 1 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148324
E;Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A;Title: Transient and restricted expression during mouse embryogenesis of D111, a murin A;Reference number: 148324
A;Accession: 148324
A;Accession: 148324
A;Residuas: preliminary; translated from GB/EMBL/DDBJ
A;Residuas: preliminary; translated from GB/EMBL/DDBJ
A;Residuas: 1-722 cRES
A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g806559; PIDN:CAA56865.1; PID:g8065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGRRSALALAVVSALLCQVWSSGVPELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A)Gene: D111
C;Superfamily: delta-4 protein; EGF homology
F;311-362/Domain: EGF homology <EGF2>
F;446-477/Domain: EGF homology <EGF>
F;446-515/Domain: EGF homology <EGF>
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121 LITEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE

1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR

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181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240 ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300 ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300

HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG

181

VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV 420

ATCINITGGGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360 ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360

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301 301 361

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Delta-4 protein - human
CJSpecies: Homo sapiens (man)
CJSpecies: Homo sapiens (man)
CJSpecies: Homo sapiens (man)
CJBCSD Homo sapiens (man)
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CJBCCSD HOMO SAPIENS (MAN)
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                                                                                                                    TCPPGFYGKNCELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSS
                                                                                                                                                                                                                                                                                  YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL
                                                                                                                                                                                                                                                                                                           532 SERHMESQGGPPPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMN
                                                                                                                                                                                                                                                                                                                                                                                                         NLANCOREKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       652 ATVRDTHSKRDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 IPPRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPD---GAGIDPAFSNPIRFPFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSYREVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLFGCDD
                                                                                                                                                                                       PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       600 NLANCQREKDISISVIGATQIKOTINKKVDFHSDN-SDKNGYKVRYPSVDYNLVHELK-NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 RSALALAVVSALLCQVW----SSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPC--ACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 TWPGTFSLIIEALHTDSPDDLATE -- NPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLR
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48.6%; Pred. No. 3.7e-109;
tive 99; Mismatches 190; Indels
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Best Local Similarity 48.6°
Matches 363; Conservative
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C.Species: dallus gallus (chicken)
C.Species: dallus gallus (chicken)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C.Jaccession: 150719
R.Henrique, D.; Adam, J.; Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
R.Title: Expression of a Delta homologue in prospective neurons in the chick.
A.Feference number: 150719; MUID:95319507; FMID:7596411
A.Accession: 150719
A.Accession: 150719
A.Accession: 150719
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-728 cHEN
A.Residues: 1-728 cHEN
A.Residues: 1-728 cHEN
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A.Residues: Efferences: UNITROCT.090656; EMBL:U26590; NID:9882411; PIDN:AAC59689.1; PID:98824
C.Superfamily: delta-4 protein; EGF homology cEGX1>
F.399-332/Domain: EGF homology cEGX2>
F.416-447/Domain: EGF homology cEGF3>
F.4492-523/Domain: EGF homology cEGF3>
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                                                                                                                                                                     VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540
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                                                                          VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG
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                                               DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP
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C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                        FSGRRCEVRITHDACASGPCFNGATCYTGLSPNNFVCNCPYGFVGSRCEFPVGLPP----
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                                                                                                                                          HGYCDKPGECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCT
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                                                                                                                                                                                                                                                                                     HHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCT
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llarity 39.9%; Pred. No. 1.3e-
Conservative 91; Mismatches
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RjMuskavitch, M.A.T.
RjMuskavitch, M.B.T.
Ajreference number: S19087
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                                               QNGYCSKPAECLCRPGWQGRLCNECIPHNGCRHGTCSTPWQCTCDEGWGGLFCDQDLNYC
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llarity 47.7%; Pred. No. 5.8e-106;
Conservative 103; Mismatches 204; Indels 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGA 493
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LLTAPICFTVIVQVHSSGSFELRLKYPSNDHGRDNEGRCCSGESDGATGKCLGSCKTRFR
                                                                                                                   SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD
                                                                                                                                                                                                 GECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN
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LCLKGYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPPSFSWPGTF
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                                                  VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGI-DPAFSNPIRFPFGFTWPGTF
                                                                                                                                                                                  EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKP
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A31246
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246
R;Kopoczynski, C.C.; Alton, A.K.; Fechtel, K.; Kooh, P.J.; Muskavitch, M.A.T.
Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes A;Reference number: A31246, MUID:89196890; PMID:3149249
A;Accession: A31246
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-832 < KOP>
A;Cross-references: GB:Y00222
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                      SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD 179
                                                                                        239
                                                                                                                                                      186 INYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGC--EHGHCDKP 243
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                                                                                                                                                                                                                     244 NQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRPCKN 303
                                                                                                                                                                                                                                                                                  304 GGTCFNTGEGLYTCKCAPGYSGDDCENEIXSCDADVNPCQNGGTCIDEPHTKTGYKCHCA 363
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     VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGI-DPAFSNPIRFPFGFTWPGTF
                                                                                                                                    EHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKP
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C;Superfamily: neurogenic protein delta; EGF
F;295-328/Domain: EGF homology «EGX1»
F;457-486/Domain: EGF homology «EGF»
F;533-564/Domain: EGF homology «EGF»
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neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)
NyAlternate names: gene D1 protein
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00670; Az6637
R;Vaession: H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMDO J. 6, 3431-340, 1987
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic A;Reference number: S00670
A;Reference number: S00670
A;Reference number: S00670
A;Residues: 1-880 <VAE>
A;Cross-references: UNIPROT: P10041; EMBL:X06289; NID:g7852; P1D:g7853
A;Ross-references: UNIPROT: P10041; EMBL:X06289; NID:g7852; P1D:g7853
A;Ross-references: UNIPROT: P10041; EMBL:X06289; NID:g7852; P1D:g7853
A;Ross-references unmber: A91081; MUD:87218537; PMID:3107986
A;Rocession: Az6637
A;Rocession: Az6637
A;Ross-references: GB:X05140; NID:g7851; P1DN:CAA28786:1; P1D:g929563
C;Generics: Doller Company A;Ross-references: GB:X05140; NID:g7851; P1DN:CAA28786:1; P1D:g929563
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A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;I-18/Domain: signal sequence #status predicted <SIG>
F;1-8/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;19-88/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>
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C;Species: Rattus norvegicus (Norway rat)
C;Dace: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
C;Accession: A56136
R;Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notchl.
A;Reference number: A56136; MUD:95211842; PMID:7697721
                                                                                                                                                                                                                                                                                                                                                                                   11 VVSALLC----QVWSSGVFELKLQEFVNKKGLLGNRNCCRG---GSGPPC--ACRIFFR
                                                                                                                                                                                                                                                                                                                     SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD
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                                                                                                                                                                                                                                             71;
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                                                                                                                                                                                           Query Match 35.5%; Score 1463.5; DB 2; Length Best Local Similarity 40.2%; Pred. No. 2.7e-83; Matches 273; Conservative 95; Mismatches 240; Indels
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R,Thomas, U.; Speicher, S.A.; Knust, E. Development 111, 749-761, 1991
A,Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a co-A,Reference number: S16148; WUID:91347903; PMID:1840519
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C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; Ā36666
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                                                                                                                                                                                                                                                                            55 -CRIFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 IRVTCDDHYYGFGCNKFCRPRDDFFGHYACDQNGNKTCMEGWMGPECNKAICRQGCSPKH
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                                                                                                                                                                                                                                                2 GRRSALALAVVSALLCQV-WSSGVFELKLQEFVNKKGLLGNRNCCR--GGSGPP--CA--
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                                                                                                                                               Length 1220;
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                                                                                                                                               Score 1312; DB 2;
Pred. No. 8.8e-74;
                                                                                                                                                                                                  78; Mismatches 215;
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A;Residues: 1-1351,'T',1353-1408 <THO2>
A;Cross-references: EMBL:X56811; NID:98563; PID:98564
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A;Residues: 1-1408 <THOL>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
R;Thomas, U.
R:Thomas, U.
R:Thomas, U.
A;Reference number: $16878
A;Reference number: $16878
                                                                                                                                               31.8%; Score 1312; 40.6%; Pred. No. 8.
A, Residues: 1-1220 <LIN>
A, Cross-references: GB:L38483
F;379-410/Domain: EGF homology <EGF1>F;492-523/Domain: EGF homology <EGF>F;634-665/Domain: EGF homology <EGF>
                                                                                                                                                                        Best Local Similarity 40.6
Matches 239; Conservative
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         30 VNECEAPHSAGIAANALLTTTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECR 589
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                                                                                                                                                                                                                               DIDECATSPCRNGGECVDMVGKFNCICPLGYSGSLCEBAKENCTPSPCLEG-HCLNTPEG 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Xenopus laevis (African clawed frog)
Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
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                                                                                                                                                                                         NVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGATCHQRGQR
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                                                                                                         TCLCRP-----GYTGRLCDNDINECL--SKPCLNGGQCTDRENGYICTCPKGTTGVNCET
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Best Local Similarity 31.6%; Pred. No. 2.1e-42;
Matches 184; Conservative 61; Mismatches 196; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: Notch protein; ankyrin repeat homology; EGF homology; Keywords: transmembrane protein; 146-177/Domain: EGF homology «EGX1»; 144-215/Domain: EGF homology «EGF1»; 222-254/Domain: EGF homology «EGF2»; 456-487/Domain: EGF homology «EGF2»; 157-788/Domain: EGF homology «EGF2»; 157-788/Domain: EGF homology «EGF2»; 157-788/Domain: EGF homology «EGF3»; 157-788/Domain: EGF homology «EGF3»; 157-788/Domain: EGF homology «EGF3»; 157-788/Domain: EGF homology EGF3»; 157-788/Domain: EGF3»; 157-788/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricoffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
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F;1025-1056/Domain: EGF homology <EGX3>
F;1924-1956/Domain: ankyrin repeat homology <AN1>
F;1957-1989/Domain: ankyrin repeat homology <AN2>
F;1951-2023/Domain: ankyrin repeat homology <AN3>
F;2024-2056/Domain: ankyrin repeat homology <AN3>
F;2057-2089/Domain: ankyrin repeat homology <AN4>
                                                                                                                                                                                                                                                                                                               YMCECAQGYGGPNCOFLLP---EPP 523
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707 YYCHCPPDRAGKHCEQLRPLCSQPP 731
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R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Teakonas, S. Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential A;Reference number: A36666; MUID:91099666; PMID:2125287
A;Accession: A36666
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15,20-26,'A',28-1408 <FLE>
A;Cross-references: GB:M35759; NID:g158605; PID:g158606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 TTAFRICLKEYQTTEQGASIS--TGCSFGNATTKILGGSSFVLSDPGVG-----AIVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFGFTWPGTFSLIIEAL -- - HTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 PPTPRWTKSFTLILQALDMYNTSYPD-----AERLIEETSYSGVILPSPEWKTLDHIGR 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 RTDLRYSYRFVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 PGCDDQHGYCDKPGECKCRVGWQGRYCDECIRYPGCVHGTCQ-QPWQCNCQEGWGGLFCN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 AGCDPVHGKCDRPGECECRPGWRGPLCNECMVYPGCKHGSCNGSAWKCVCDTNWGGILCD 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 TSNRTQAQVYRTSHGRSNMGRPVRRSSSMRSLDHLRPEGQALNGSSSSGLVSLGSLQLQQ 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGKVCELS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 QLAPDFTCDCAAGWTGPTCEINIDECAGGPCEHGGTCIDLIGGFRCECPPEWHGDVCQVD 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----ADGPCFNGGRCS 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPP-----CA-C 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.4%; Score 1130; DB 2; Length 1408; Best Local Similarity 33.0%; Pred. No. 1.9e-62; Matches 226; Conservative 72; Mismatches 197; Indels 190;
                                                                                                                                                                                                                                                                                                               A,Gene: FlyBase:Ser
A,Coses-references: FlyBase:FBgn0004197
A;Croses-references: FlyBase:FBgn0004197
C;Keywords: glycoptocein; transmembrane protein
F;1-84/Domain: signal sequence #status predicted <SIG>F;1-408/Froduct: gene serrate protein #status predicted <MAT>F;85-1221/Domain: extracellular #status predicted <EXT>F;85-1221/Domain: extracellular #status predicted <EXT>F;85-121/Domain: EGF homology <EG01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ir homology <EG01>
Fr homology #status atypical <EG04>
Fr homology #status atypical <EG06>
Fr homology #status atypical <EG06>
Fr homology <EG07>
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homology <EG02>
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homology <EG14>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:883-914/Domain: EGF | F:921-952/Domain: EGF | F:997-1060/Region: cyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;615-645/Domain: E
F;622-683/Domain: E
F;690-70/Domain: E
F;727-796/Domain: E
F;803-834/Domain: E
F;841-876/Domain: E
F;893-914/Domain: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;319-348/Domain:
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F;495-526/Domain:
F;533-608/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286
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971 CPVĞFNĞIHCENNTPDCTESSCFNĞGTCVDGINSFTCLCPPGFTGSYCQYDVNECDSRPC 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----CDSGTCLDKIDGYECACEPGYTGSMCNVNIDEC 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 AGSPCHNGGTC---EDGIAGFTCRCPEGYHDPTCLSEVNECNSNPCIHGACRDGLNGYKC 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -CDPGWKGOYC-----TDPICLPG--CDDQ-HGYCDKPGECKCRVGWQGRYC---D 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCIRYPGCVHGTC------00PW 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 OCNCOEGWGGLFCNODLNYCTHHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDEC 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCVCPTGWQQTCEVDINECV-KSPCRHGASCQNT-NGSYRCLCQAGYTGRNCESDIDDC 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 ANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYG 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECASNPCLNQGTCIDDVAGYKCNCPLPYTGATCEVVLAPCATSPCKNSGVCKESEDYESF 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 APSPCKNGASCTDLEDSFSCTCPPGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCH 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPNCQFLLPE-------PPPGPMVVDLSERHMESQGGPFPWVAVCAGVVLVL 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRGGS----GPPCACRTFFRVCLKHYQAS-----VSPEPPCTYGSAVTPVLGVDSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LPDGAG-----IDPAFSNPIRFPFGFTWPGTFS-----LIIEALHTDSP------DDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 QPGYTGHHCETNINECHSQPCRH-----GGTCQDRDNSYLCLCLKGTTGPNCEINLDDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GDRGEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537 CKNGAKCLDGP----NTYTCVCTEGYTGTHCEVDIDECDPD-PCHYGSCKDGVATFTCLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDEHYYGEGCSV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1091 ĠVNĊDVLSVSCEVAAQKRGIDVTLLCQHĠGLCVDEGDKH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.6%; Score 807.5; DB 2; 28.3%; Pred. No. 3e-42; tive 60; Mismatches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            < AN4 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <AN3>
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F;1063-1094/Domain: EGF homology <EGI6>
F;1149-1180/Domain: EGF homology <EGI7>
F;1187-1218/Domain: EGF homology <EGI8>
F;123-1264/Domain: EGF homology <EGF8>
F;1352-1383/Domain: EGF homology <EGF9>
F;1391-1425/Domain: EGF homology <EGF9>
                                                                                                                                                                                                                                                                                                                                                                                       homology <EG14>
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EGF homology RGF h
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Best Local Similarity 28.3%
Matches 223; Conservative
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          :416-449/Domain:
                                                                                                                                             F;607-638/Domain:
                                                                                                                                                                         F;682-713/Domain:
                                                                                                                                                                                                                F;757-788/Domain:
                                                                                                                                                                                                                                                795-826/Domain:
                                                                                                                                                                                                                                                                                    F;873-904/Domain:
                                                                                                                                                                                                                                                                                                                911-942/Domain:
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                                                                          ;494-525/Domain:
                                                                                                             /Domain:
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R; Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.; submitted to the EMBL Data Library, April 1992
A; Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggest A; Reference number: S25144
A; Accession: S25144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         betwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nictorate names: motch protein
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 16-Aug-2004
C;Accession: A46019; S25144; C49175; B46438; A46438; PHI569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Gric
Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A;Reference number: A46019; MUID:93194170; PMID:8449489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-2531 <DEL>
A;Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
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A,Reference number: A46438; MUID:93252998; PMID:8486742
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A;Residues: 1865-1932,'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',205<
A;Experimental source: embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1551-2108, 'Q',2110-2114,'ALP',2118-2170 <FRA>
A;Cross-references: EMBL:211886
R;Leadelll, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
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C;Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
C;Comment: This protein is one of the neurogenic proteins controlling the decision
                                                                                                                                                                                                                                             CFNGGTCIDGINTFTCQCPPGFTGSYCQHDINECDSKPCLNGGTCQDSYGTYKCTCPQGY 1051
                                                                                                                                                                                                         472
   -NRPCRNGATCQNT-NGSYKCNCKPGYTGRNCEMDIDDCQPNPCHNGGSCSDGINMFFCN 932
                                                                   CPPGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSP 412
                                                                                                                                          991
                                                                                                          CPAGFRGPKCEEDINECASNPCKNGANCTDCVN-SYTCTCQPGFSGIHCESNTPDCTESS
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A;Residues: 1161-1547 «LAR»
A;Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988
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rotein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                       TGKNCSAPVSRCEHAPCHNGATCHQRGORYMCECAQGYGGPNC 515
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A; Note: sequence extracted from NCBI backbone (NCBIP:126159)
R; Kopan, R.; Weintraub, H.
J. Cell, Biol. 121, 631-641, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Status: preliminary; nucleic acid sequence not shown
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F;222-254/Domain: EGF homology «EG72»
F;261-292/Domain: EGF homology «EG02»
F;339-370/Domain: EGF homology «EG03»
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notch-1 protein - mouse
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C, Superfamily: Notch pr
F, 106-138/Domain: EGF?
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the uEGF gene in the sea urchin Strongylocentrotus purpuzi:90112459; PMID:2514273
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):89196806; PMID:2784773
                         ASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAP 488
                                                                                                                                                                                     -----YCHCQAGYTGSYCEDEVDECSPNPC-----QNG 1157
                                                                                                                                                                                                                                                                                                                                                  AOGYGGPNCOFLLPE------PPPGPMVVDLSE 533
                                                                                                                                                                                                                                            VVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNL 593
                                                                                                                                                                                                                                                                                                                             IKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGD--- 650
GYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVDLGNSYLC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rongylocentrotus purpuratus)

owth factor homolog precursor

ed fibropellin Ib (EGFI)

urpuratus (purple urchin)

vision 17-Sep-1997 #text_change 09-Jul-2004

1016; A29316; A43131

lo, D.R.; Hursh, D.A.; Raff, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <HUR>
ID:9161474; PIDN:AAA30050.1; PID:9552260
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homology (C1R)
eEG02>
eEG03>
eEG04>
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aff, R.A.
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-247 * SBLS
A;Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA48831.1; PID:g4338
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: notch protein; acgrain: EGF homology ceGF2
F;1023-1054/Domain: EGF homology ceGF2
F;1915-1947/Domain: ankyrin repeat homology caN1>
F;1948-1980/Domain: ankyrin repeat homology caN3>
F;1961-2044/Domain: ankyrin repeat homology caN3>
F;2015-2044/Domain: ankyrin repeat homology caN3>
F;2015-2044/Domain: ankyrin repeat homology caN3>
F;2015-2040/Domain: ankyrin repeat homology can3>
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                                                   pattern
                 Mech. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its
A;Reference number: S42612; MUID:94128602; PMID:8297791
A;Accession: S42612
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N;Alternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Dapeide: Mus musculus (house mouse)
C;Accession: A49175; PHI570; S32113
R;Lardelli, M.; Lendahl, U.
Bxp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a winkReference number: A49175; MUID:93178563; PMID:8440332
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        C.; Campos-Ortega, J.A.
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                                                                                                                                                                                                                                                                                                                                                      F;23-34, 28-43, 45-54, 62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-27,451-466,468-477,488-495/Distulfide bonds: #status predicted
F;489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-62
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Distul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCDEHYYGEGCSV-----FCRPRDDAFGHFTCGDRGE-----KMCDPGWKGQYC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 ICIDGINGYTCSCPLGFSGDNCENNDDECSSIPCLNGGTCVDLVNAYMCVCAPGWTGPTC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 ADNIDECASAPCQNGGVCIDGVNGYMCDCQPGYTGTHCETDIDECARPPCQNGGDCVDGV 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYCTHHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDS 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPCINGGACMDVVNGFVCTCLPGWEGTNCEINTDECASSPCMNGGLCVDQVNSYVCFCL 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGYVCI CAPGFDGINCENNI DECASRPCONGAVCVDGV--NGFVCTCSAGYTGVLCETDI 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NECA-SMPCLNGGVCTDLVNG-YICTCAAGFEGTNCETDTDECASFPCQNGATCTDQVNG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVDLGNSYLCRCQ 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPC--GGE-TETMNNL------ANCQR 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGESGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPVSRCEHAPCHN 491
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transmembrane protein precursor - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S42612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CRVGWQGRYC----DECIRYP-----GCVHGTCQQPWQCNCQEGWGGLFCNQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%; Score 771; DB 2; Length 1064;
larity 31.8%; Pred. No. 2.5e-40;
Conservative 45; Mismatches 188; Indels 140;
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                         EGF homology
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F;332-363/Domain: E
F;370-401/Domain: E
F;446-477/Domain: E
F;544-515/Domain: E
F;522-551/Domain: E
F;560-591/Domain: E
F;560-591/Domain: E
F;636-667/Domain: E
F;674-705/Domain: E
F;770-781/Domain: E
F;750-781/Domain: E
                                                                                                                                                                                                                                                                                                                                   F;936-1064/Region:
                                                                                                                                                                                                                                                                    F;826-857/Domain:
F;864-895/Domain:
F;902-933/Domain:
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Matches 174;
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A; Molecule type: mRNA
A; Residues: 1-1203 <LAR>
A; Residues: 1-1203 <LAR>
A; Residues: 1-1203 <LAR>
A; Cross=references: UNIPROT: 035516; EMBL: X68279; NID: 9287989; PIDN: CAA48340.1; PID: 92879
A; Cross=references: uniprot: embryo
A; Note: sequence extracted from NCBI backbone (NCBIP: 126158)
C; Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C; Comment: This protein is one of the neurogenic proteins controlling the decision betwe C; Superfamily: Notch protein; ankfyrin repeat homology; EGF homology
F; 143-174/Domain: EGF homology <EGX1>
F; 842-513/Domain: EGF homology <EGX2>
F; 650-512/Domain: EGF homology <EGY2>
F; 674-705/Domain: EGF homology <EGX3>
F; 812-743/Domain: EGF homology <EGX3>
                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----IDPAFSNP----IRPPFGF---TWPGTFSLIIEALHTDSPDDLATENP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 YMGAICSDQIDECYSSPCLNDGRCIDLVNGYQCNCQPGTSGLNCBI----NFDDCAS-NP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 CMHGVCVDGINRYSCVCSPGFTGQRCNIDIDECASNPCRKGATCINDVNGFRCICPEGPH 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 GEGCSV---FCRPRDDAFGHFTCGDRGEK-MCDPGWKGQYC-----TDPICLPG--C 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 HPSCYSQVNECLSNPCIHGNCTGGLSGYKCLCDAGWVGVNCEVDKNECLSNP-CQNGGTC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456 NNLVNGY-----RCTCKKGFKGYNCQVNIDECASNPCLNQGTCFDDVSGYTCHCMLPYTG 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----OQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGA 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 LNGAKCIDHPNGYECQCATGFTGILCDENIDNCDPDPCHHGOCQD---GIDSYTCICNPG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 -----ERLISR-----LTTQRHLTVGEEWSQDLHSSGRTDLR--YSYRFVCDEHYY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DD-QHGYCDKPGECKCRVGWQGRYC----DECIRYPGCVHGTC------- 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 TCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGKV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVD 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 LGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAPV 481
                                                                                                                                                                                                                                                                                                                                                      18.5%; Score 761; DB 2; Length 1203;
32.2%; Pred. No. 1.2e-39;
tive 61; Mismatches 216; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 LGNRNCCRGGSGPPCACRTFFRVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 SRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFL 518
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Best Local Similarity 32.2%
Matches 186; Conservative
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GenCore version 5.1.6
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- protein search, using sw model OM protein

November 29, 2004, 13:12:09 ; Search time 86.9238 Seconds (without alignments) 4779.132 Million cell updates/sec Run on:

US-09-783-931-12 4121

1 MGRRSALALAVVSALLCQVW......YQSVYVLSAEKDECVIATEV 722 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Ofofv7 mus musculu			Aah65063 mus muscu	Q61483 mus musculu	P97677 rattus norv	O00548 homo sapien	-	Q91902 xenopus lae	~	4	P87357 brachydanio	Q6di48 brachydanio	O57462 brachydanio	Q7zxt4 xenopus lae		homo	_	mus	Q9iat6 brachydanio		Q8i498 cupiennius		-			Q6t4n2 drosophila		_	Aar21454 drosophil	-
SOUTHWENTES	ID	O6PFV7	AAH57400	AAR30869	AAH65063	DLL1 MOUSE	DLL1_RAT	DLL1 HUMAN	Q906 <u>5</u> 6	091902	Q8AW87	Q8UWJ4	P87357	Q6D148	057462	Q7ZXT4	P79941	DLL4_HUMAN	DLL4_MOUSE	<u> </u>	Q9IAT6	057409	Q81498	Q7Q0MS	Q6T4M9	Q6T4N0	Q6T4N1	Q6T4N2	Q6T4N6	AAR21453	AAR21454	AAR21461
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*	Query Match	97.2	97.2	97.2	97.2	97.1	93.4	98.6	81.7	76.9	76.3	68.6	68.5	7.	65.8	46.2	46.0		44.5	44.4	43.9			35.7	35.7	35.7	35.7	35.7	35.7		35.7	35.7
	Score	4007	4007	4007	4007	4003	3848	3652.5	3368	3167.5	3146	2826.5	2823.5	2778	2713	1902	1896	1879.5	1832	1828	1810.5	1775.5	1630.5	1472	1469.5	1469.5	1469.5	1469.5	1469.5	469.		1469.5
	Result No.		8	٣	4	ß	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

Strausberg R.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

[3] SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Mouse;

SEQUENCE FROM N.A. STRAIN=CS7BL/6J; Nagaraja R., Weeltz P., Brathwaite M.E.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

[5] SEQUENCE FROM N.A.

Strausberg R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

HÄÄ	Aar21460 drosophil Aar21465 drosophil
AAR21462 AAR21464 AAR21464 DL DROME Q6T4N3 Q6T4N3 AAR21455 AAR21456 AAR21457 AAR21459 AAR21459	AAR21460 AAR21465
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ALIGNMENTS

RESULT 1 OGFFV7 D OGFFV7
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STRAIN-C57BL/6; TISSUE=Mouse;

STRAIN-C57BL/6; TISSUE=Mouse;

STRAIN-C57BL/6; TISSUE=Mouse;

MEDLINE=2238825; PubMed=12477932;

STRAIN-C57BL/6; TISSUE=Mouse.

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Alsechul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhar N.K.,

Alsechul S.F., Zeoberg B., Buetcow K.H., Schaefer C.F., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stopelecon M.J., Soates M.B., Toghinyla, S., Carninci P., Prange C.,

Romangelecon M.J., Ugdin T.B., Toghinyla, S., Carninci P., Prange C.,

Romangelecon M.J., McKernan K.J., Malek J.A., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Maramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;
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                                                                                                                             RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCG57400; AAH57400.1; -
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
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AAH57400;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Delta-like 1.
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STRAIN-C57BL/6; TISSUE=Mouse;
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STRAINE-CYBL/BU/POL)

STRAINE-CYBL/BU/POL)

SUBMITTED TW. Waeltz P., Dudekula D., Nagaraja R.;

Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.

"I SIMILARITY: Contains 8 EGF-like domains.

EMBL; BC05-000 AAH57400 1; -

EMBL; BC065063; AAH65063.1; -

EMBL; BC065063; AAH65063.1; -

EMBL; BC065063; AAH65063.1; -

EMBL; BC067000386; F:Prortein binding; IPI.

GO; GO:0007386; F:Prortein binding; IPI.

GO; GO:0007386; F:Prortein binding; IPI.

GO; GO:0007386; F:Prortein binding; IPI.

GO; GO:000173; F:Prortein ESCIFication; IMP.

RO; GO:000174; EGF 2.

INTERPRO: IPRO0189; EGF 2.

INTERPRO: IPRO0189; EGF 2.

INTERPRO: IPRO0189; EGF 2.

INTERPRO: IPRO0189; EGF 1.

EMM. PF001081; EGF 6.

PEAM; PRO0109; EGF 6.

PEAM; PRO0109; EGF 6.

PEAM; FROO109; EGF 6.

PEAM; FROO109; EGF 6.

PEAM; PRO0109; EGF 6.

PEAM; PRO0109; EGF 7.

SWART; SW00011; EGF 8.

SWART; SW0011; EGF 8.

SWART; SW00119; EGF 7.

PROSITE; PS00109; EGF 7.

PROSITE; PS001186; EGF 7.

PROSITE; PS001186; EGF 7.

PROSITE; PS001186; EGF 7.

PROSITE; PS001186; EGF 7.

PROFITE; PS001187; EGF 7.

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                                                                                                    VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS
                                                                                                                                       LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE
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AAH65063;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
              ö
              Indels
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
               16;
 ed. No. 4.6e-269;
Mismatches 16;
  97.4%; Pred. No.
             3;
             Conservative
Best Local Similarity
Matches 703; Conserv
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               LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
VCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagaraja R., Waeltz P., Brathwaite M.E.; "Genomic Sequence Analysis in the Mouse t-complex Region."; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J;
Brathwaite M., Waeltz P., Dudekula D., Nagaraja R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY491019; AAR30869.1; -.
SEQUENCE 722 AA; 78449 WW; 9D570B9DC7EEC75E CRC64;
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STRAIN=C57BL/6J;
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EMBL; X80903; CAA56865.1; -. PIR; I48324; I48324.
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bronstein M.J., Uddin T.B., Toshiyuki S., Carninol P., Prange C.,
A Rhaha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Holards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Goneration and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                              97.2%; Score 4007; DB 2; 97.4%; Pred. No. 4.6e-269;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                          703; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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SEQUENCE FROM N.A.

STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;

XX MEDINE=55401858; PubMed=7671806;

Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;

Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;

Transient and restricted expression during mouse embryogenesis of

TIL, a murine gene closely related to Drosophila Delta.";

Development 121:2407-2418 (1995).

In Charlow. May be involved in cell-to-cell communication in

mammalian embryos. May have a role in cellular interactions

underlying somitogenesis and development of the nervous system.

In SUBUNIT: Interacts with Notch receptors.

In SUBCELLULAR LOCATION: Type I membrane protein.

In TISSUE SPECIFICITY: In the embryo, expressed in the paraxial

mesoderm and nervous system. Expressed at high levels in adult

heart and at lower levels, in adult lung.

In DERCOMMENTAL STAGE: Expressed until day 15 in the embryo.

Expression then decreases and increases again in the adult.

IN SIMILARITY: Contains 1 DSL domains.
                                                                                                 RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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R GO; GO:0005576; C:extracellular; ISS.

R GO; GO:0005887; C:integral to plasma membrane; ISS.

R GO; GO:000512; F:Notch binding; IPI.

R GO; GO:000512; F:Notch binding; IPI.

R GO; GO:0007386; P:cell fate determination; ISS.

R GO; GO:0007386; P:cell fate determination; ISS.

R GO; GO:0007386; P:cell fate commitment; IMP.

R GO; GO:0007386; P:hair cell fate commitment; NAS.

R GO; GO:0009912; P:hair cell fate commitment; NAS.

R GO; GO:0007399; P:neurogeneeis; ISS.

R GO; GO:0007399; P:neurogeneeis; NAS.

R GO; GO:0007399; P:neurogeneeis; NAS.

R GO; GO:0007219; P:Notch signaling pathway; ISS.

R GO; GO:0007219; P:Notch signaling pathway; ISS.

R GO; GO:0007219; P:regulation of cell adhesion; ISS.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-2094 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Dishibto G., Hebshi L., Boulter J., Weinmaster G.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system similarity)
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-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SIMILARITY: Contains 1 DSL domain.
-:- SIMILARITY: Contains 8 EGF-like domains.
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PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS01021; EGF 1; 8.
PROSITE; PS01086; EGF 2; 8.
PROSITE; PS01087; EGF 2; 8.
PROSITE; PS01087; EGF 3; 7.
PROSITE; PS01087; EGF 3; 7.
PROSITE; PS01087; EGF CA; 2.
PROSITE; PS01087; EGF CA; 2.
REPEAT, Signal; Transmembrane.
3 I Potential.
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Extracellular (Potential)
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Asx_hydroxyl_S.
                                             InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF II.
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                          8;
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77378 MW; 4B8EE2272BAEA27E CRC64;
                                                        Query Match 93.4%; Score 3848; DB 1; Best Local Similarity 93.2%; Pred. No. 4.7e-258; Matches 673; Conservative 13; Mismatches 28;
   714 AA;
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CG) GG: 0005587; C: cintegral to plasma membrane; ISS.

CG) GG: 00051576; C: cintegral to plasma membrane; ISS.

CG) GG: 0005154; P: Nocch binding; Pr.

CG) GG: 0001709; P: cell differentiation; ISS.

CG) GG: 0001709; P: cell fate determination; ISS.

CG) GG: 0001709; P: pelmatr cell fate commitment; NAS.

CG) GG: 0001709; P: pelmatr cell fate commitment; NAS.

CG) GG: 0001709; P: pelmatr cell fate commitment; NAS.

CG) GG: 0001709; P: pelmatr cell fate commitment; NAS.

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Delta-like protein 1.
Extracellular (Potential)
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Cytoplasmic (Potential)
         EMBL, U78889; AAB37343.1;
HSSP, P08709; 1BF9.
RGD; 70949; D111.
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EGF-like 6.
EGF-like 6.
EGF-like 7.
CGF-like 6.
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PROSITE; PS00012; EGF 1; 8
PROSITE; PS00186; EGF 2; 8.
PROSITE; PS01186; EGF 3; 7.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
Sevent; Signal; Transmembrane.
SIGNAL
           MIM; 606582; -. Governace||ular; NAS.
GO; GO:0005576; C:extrace||ular; NAS.
GO; GO:0005876; C:integral to plasma membrane; NAS.
GO; GO:000512; F:Notch binding; IFT.
GO; GO:000312; F:Notch binding; IFT.
GO; GO:000312; F:Notch binding; IFT.
GO; GO:000312; P:cell differentiation; TAS.
GO; GO:0003912; P:hair cell fate determinent; ISS.
GO; GO:0003912; P:hair cell fate commitment; ISS.
GO; GO:0003912; P:hair cell fate commitment; ISS.
GO; GO:0003912; P:hair cell fate commitment; ISS.
R GO; GO:000392; P:neurogenesis; ISS.
R GO; GO:0003129; P:neurogenesis; ISS.
R GO; GO:0003129; P:neurogenesis (sensu Vertebrata); ISS.
R GO; GO:000312; P:regulation of cell adhesion; TAS.
InterPro; IPR00112; Asx hydroxyl_S.
R InterPro; IPR00112; Asx hydroxyl_S.
R InterPro; IPR00181; EGF_Ca.
DR InterPro; IPR00181; EGF_Ca.
DR InterPro; IPR00183; EGF_II.
DR Pfam; PR01414; DSL; 1.
DR Pfam; PR00100; EGFBLOOD.
BR SWART; SM0012; EGFBLOOD.
BR SWART; SM0012; EGF CA; 4.
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Extracellular (Potential)
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21464863; PubMed=11581320;
A Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M., Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M., Henrique D., Parreira L.;
A Henrique D., Parreira L.;
I Differential effects of Notch ligands Delta-1 and Jagged-1 in human lymphoid differentiation.";
J. Exp. Med. 194:991-1001(2001).
L. Exp. Med. 194:991-1001(2001).
C. I- FUNCTION: Acts as a ligand for Notch receptors. Blocks the differentiation of progenitor cells into the B-cell lineage while promoting the meregence of a population of cells with the characteristics of a T-cell/NK-cell precursor.
C. I- SUBUNIT: Interacts with Notch receptors.
C. I- SUBCHICITY: Expressed in heart and pancreas, with lower expression in brain and muscle and almost no expression in placenta, lung, liver, and kidney.
C. I- SIMILARITY: Contains B EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
MEDLINE-22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
A Chen J., Chow B., Chui C., Crowley C., Currell B., Dowd P.,
B Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
A Huang A., Kim H.S., Klimenoski L., Jin Y., Johnson S., Lee J.,
Beshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagets A.,
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The secreted protein discovery initiative (SPDI), a large-scale
effort to identify novel human secreted and transmembrane proteins: a
ferome Res. 13:2265-2270(2003).
                                                                                                           s:
[1] SEQUENCE FROM N.A. MEDINEG=10079256; MEDINEE=9180765; PubMed=10079256; Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Gram Ann A., Ward D., Ish-Horowitz D., Artavanis-Teakonas "Human ligands of the Norch receptor."; Am. J. Pathol. 154:785-794(1999).
                                                                                                                                                                                                         SEQUENCE FROM N.A.
Han W., Ye Q., Moore M.A.S.;
"A soluble form of human delta-like-1 inhibits differentiation of
                                                                                                                                                                                                                                                                                            hematopoietic progenitor cells.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Oda T., Chandraeskharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Almeida J.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AF186571; AAF05834.1; --
EMBL; AF222210; AAG09716.1; --
EMBL; AY358892; AAG089251.1; --
EMBL; AL078605; CAB89569.1; --
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. .) (Potential).

-linked (GlcNAc. . .) ()
-> Q (in Ref. 2).
-> R (in Ref. 4 and 5)
-> S (in Ref. 2).

CONFLICT CONFLICT CONFLICT

HSSP; P00740; 1EDM. Genew; HGNC:2908; DLL1.

EMBL; HSSP;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THHKPCRNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 CDCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 YSYRFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 YNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACRTFFRVCLXHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGA-GIDPAFSNPIRFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCPPGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCSNGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTGKNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                           Lewis J., Ish-Horowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
            TISSUE-Spinal cord;
MEDLINE-95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowi
"Expression of a Delta homologue in prospective neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGRRSALALAVVSALL--CQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                      728 AA; 79861 MW; 93B2D6666D238BB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.7%; Score 3368; DB 2; 1
llarity 78.5%; Pred. No. 8.3e-225;
Conservative 73; Mismatches 72;
                                                                                                                                      ASSI, 700/10/10, Cimembrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:00071509; F:calcium ion binding; IEA.
GO; GO:0007151; BEA.
InterPro; IPR001774; DSL.
InterPro; IPR00174; DSL.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_Li.
InterPro; IPR00181; EGF_Li.
PFam; PP01010; EGFBLCOD.
SWART; SW00010; EGFBLCOD.
SWART; SW00010; EGFBLCOD.
SWART; SW00010; EGF CA; 4.
PROSITE; PS00100; EGF CA; 4.
PROSITE; PS01186; EGF_2; 8.
                                                                                  Nature 375:787-790(1995).
EMBL; U26590; AAC59689.1;
PIR; I50719; I50719.
HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
574; Conserv
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                                                                                                                                                                                                     SLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCD
                                                                                                                                                                                                                      GATCINTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYG
                                                                                                                                                                                                                                                                                                                                                                                          090656 PRELIMINARY, PRT; 728 AA.
090656,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
C-Delta-1.
Gallus (Chicken).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
[1]
                                                                                                   60 RVCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTF
                                                                                                                                                                                                                                                                                                                      GECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRN
                                                                                                                                                                                                                                                                                                                                                                                                                                      KVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHS
                                                                                  1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSG-PPCACRTFF
                                                         Gaps
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Э
                            DB 1; Length 723;
                                                         46; Indels
77956 MW; B4EC455FFA32A12B CRC64;
                         88.6%; Score 3652.5; DB 1
86.9%; Pred. No. 1.6e-244;
ive 46; Mismatches 46;
                                                      Matches 629; Conservative
Ź
                                        Local Similarity
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SEQUENCE
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                            Query Match
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090656
10
090656
AC 0906
DT 01-N
DT 01-N
DT C-M
DE CA-DE
OC BURA
OC ARCH
OC GAILL
OX NCBI
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180

237 240

177

297 300 357 360 420 477 480 537

417

598

657 657

538 597

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658 RSKCEAKCSSNDSDSEDVNSVHSKRDSSE-----RRRPDSAYSTSKDTKYQSVYVI 708
                                                                                                                                 361 YGKNCELSAMTCADGPCFNGGRCADNPDGGYICFCPVGYSGFNCEKKIDYCSSNPCANGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCPPGYIGKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 GQSGQFPWIAVCAGIVLVLMLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMMNLANCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MGQQRMLTLLVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSLASLQRCECKT
                                                                                                                                                                                                                                                        238 KPGECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC
                                                                                                                                                                                                                                                                                                                               298 RNGATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQGGPPPWAVCAGWLVLLLLLGCAAVWCVRLKLQKHQPPPEPCGGETETWNNLANCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSKRDTKCQS-----QSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVL
                                                                                                              118 TFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFV
                                                                                                                                                                                     CDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCD
                                                                                                                                                                                                                                                                                                                                                                                                      YGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cynops pyrrhógaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saito T.;
databases.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ligand Delta-1.
Name=Delta-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
Nakamura K., Kikuchi Y., Susaki K., Chiba C.,
Nakamura K., Kikuchi Y., Susaki K., Chiba C.,
Sumitted (OCT-2002) to the EMBL/GenBank/DDBJ
-1- SIMILARITY: Contains 8 EGF-like domains.
EMBL, AB055017; BAC41350.2; -.
HSSP, P00740; 1EDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
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SDEKDECIIATEV 721
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SEQUENCE FROM N.A.

MEDLINE=95319503; PubMed=7596407;

A Chituia A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

Thituia A., Henrique D., Lewis J., Ish-Horowicz D., Kintner C.;

The Drosophila neurogenic gene Delta.";

The Drosophila neurogenic gene Delta.";

Rubl.; 142229; AAC38017.1;

Rubl.; 142229; AAC38017.1;

Rubl.; 142229; Pac38017.1;

Rubl.; 15A222; Pac38017.1;

Rubl.; 15A2225; Pac38017.1;

Rub
:|::| | | |||:|||||:|||:||| TEKYTEGQNSQFPWIAVCAGIILVLMLLLGCAAIVVCVRLKVQKRHHQPEACRSETETWN
                                                                                                                                                 NLANCQREKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDE
                                                                          -CACRT
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                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
VCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.9%; Score 3167.5; DB 2; Length 721; 72.9%; Pred. No. 6.2e-211; tive 89; Mismatches 87; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;
                                                                                                                                                                                                                                                                                                                                          Q91902;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
X-Delta-1.
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EKDECIIATEV 728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINES-22248969; MEDLINES-22248969; PubMed=12361969; Hans S., Campos-Ortega J.A.; "On the organisation of the regulatory region of the zebrafish deltab
                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DeltaD proctein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Annio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NCBL TaxID=7955;
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GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0007154; P:call communication; IEA.

InterPro; IPRO01774; DSL.

InterPro; IPRO01774; DSL.

InterPro; IPRO0174; DSL.

InterPro; IPRO01438; EGF Z.

PRUNTS; PRO0100; EGFBLCOD.

SMART; SM00051; DSL; 1.

PROSITE; PS01001; EGF Z; 8.

PROSITE; PS01186; EGF Z; 8.

PROSITE; PS01187; EGF Z; 8.

PROSITE; PS01187; EGF Z; 8.

PROSITE; PS01187; EGF Z; 8.
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EMBL; AF426384; AAL31528.1; -.
HSSP; P00740; 1EDM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSER 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            535 HMESQGGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQK-HQPPPEPCGGETETMNNL 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        726 AA; 79866 MW; 352A40219AE67F41 CRC64;
GO; GO:0007154; P:cell communication; IEA.
InterPro; IPR000152; Aax_hydroxyl_S.
InterPro; IPR001774; DSL.
InterPro; IPR001774; DSL.
InterPro; IPR00143; EGF_Z.
InterPro; IPR001439; EGF_II.
InterPro; IPR001439; EGF_II.
InterPro; IPR006210; IEGF.
Pfam; PF00414; DSL; 1.
Pfam; PF00414; DSL; 1.
Pfam; PF00010; EGFBLODD.
SMART; SM00010; EGFBLODD.
SMART; SM00191; EGF 6, 6.
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00102; EGF_Z; 7.
PROSITE; PS01186; EGF_Z; 7.
PROSITE; PS01187; EGF_Z; 7.
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                                                                                                                                                                                                                                                                                                                                           KNCTSAVNKCLHNPCHNGATCHEMDNRYVCACIPGYGGRNCQFLLPENPQGQAIVEGADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RYSYEEDDGGFPWTAVCAGIILVLLVLLVLSSSSVFVIYIRLKLQQRSQQID-SHSEIETWNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGRRSALALAVVSALLC---QVWSSGVFELKLQEFVNKKGLLGNRNCCRGGS--GPPCA
                                                                                                                                                                                                                                                                                                                          CRIFFRUCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRPPFGFT
                                                                                                                                                                                                                                                                                                                                                                                                 WPGTFSLIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RFVCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGFYGKVCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGAKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H--MESQGGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATVRDTHSKRDTKCQSQSLQEKRRSPQHL---GVGRFLTENRPESVYSTSKDTKYQSVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: |||: ||||||||||:|
LGKEDSERSEATKCEPLDSDSEERHRNHLKSDSSERKRTE-----SLCKDTKYQSVFV
                                                                                                                                                                                                                29;
                                                                                                                                                                               2; Length
                                                                                                                                                                                                                  Indels
                                                                                                                          Potential.
9C5A0162504593E4 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                           68.5%; Score 2823.5; DB 2; 66.3%; Pred. No. 4.1e-187; ative 98; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
PROSITE; PS00010; ASX HYDROXYL; 3.
PROSITE; PS00022; EGF 1; 8.
PROSITE; PS01186; EGF 2; 8.
PROSITE; PS50026; EGF 3; 6.
PROSITE; PS01187; EGF CA; 2.
EGF-like domain; Signal; Transmembrane.
                                                                                                                                                                                                                Conservative 98;
                                                                                                                                         717 AA; 79061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28,
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Best Local Similarity
Matches 487; Conserv
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Q6D148;
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01-OCT-2004 (
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                                                                                                                                                                         KNCSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSER
                                                                                                                                                                                                                                                                                                                          H--MESQGGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNN
                                                                                                                                                                                                                                                                                                                                                                                                LANCQ-REKDVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDE
                                                                                                                                                                                                                                                                                                                                                                                                                  neurogenic
somitic
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01-MAY-1997 (TrEMBLrel. 03, Loat aguence update)
01-MAR-2097 (TrEMBLrel. 03, Last sequence update)
01-MAR-2097 (TrEMBLrel. 26, Last annotation update)
01-MAR-2097 (TrEMBLrel. 26, Last annotation update)
Deltab transmembrane protein precursor.
Name=1dd; Synonyms-deltab;
Name=eldd; Synonyms-deltab;
Netacoa, Cabrafish) (Danio rerio).
Eukaryota; Metacoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Oyprinidae; Danio.
NCBL_TAXID=7955;
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MEDLINE=97804 N.T.

MEDLINE=97804 N.T.

Dornseifer P., Takke C., Campos-Ortega J.A.;

Dornseifer P., Takke C., Campos-Ortega J.A.;

Dornseifer P., Takke C., Campos-Ortega J.A.;

T. Overexpression of a zebrafish homologue of the Drosophila neur gene delta perturbs differentiation of primary neurons and somil development.";

Development.";

Mech. Dev. 63.159-171(1997).

EMBL; Y11760; CAA72425.1; -.

EMBL; Y11760; CAA7425.1; -.

EMBL; SMO010; EGFELOD.

EMART; SMO0179; EGF_CA; 4.
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LSEEKDECIIATEI 717
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P87357
ID P87357
ID P87357
AC P8735
AC
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420 ARCVDLVNSYLCQCPDGFTGMNCDRAGDECSMYPCQNGGTCQEGASGYMCTCPPGYTGRN 479
                                                                                            CSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQPLLPEPPPGPMVVDLSERHM
                                                                               537 ESQGGPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQ--KHQPPPEPCGGETETMNNLA
                                                                                                                                                                                   ------GDEATVRD--THSKRDTKCQ----SQSLQEKRR-----SPQHLG
                                                                                                                                595 -NCOREKDVSVSIIGATQIKNTNKKADFHGDHG----AEKSSFKVRYPTVDYNLVRDLK
                                                                                                                                                                                                                                     682 VGRFLTENRPESVYSTSK-------DTKYQSVYVLSAEKDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name-cla; Synonyms-deltaA;
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cypriniformes;
Cyprinidae; Danio.
NCBI_TAXID=7955;
                                              480 CSSPVSRCQHNPCHNGATCHERNNRYVCACVSGYGGRNCQFLLPD------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDINE=9915133; MEDINE=99165392; PubMed=9425133; Appel B., Eisen J.S.; Regulation of neuronal specification in the zebrafish spinal obelta function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0D8A9734585918E5 CRC64;
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Last annotation update)
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GO; GO:0005509; F:callcium ion binding; IEA.
GO; GO:0007519; F:callcium ion binding; IEA.
GO; GO:0007154; P:call communication; IEA.
InterPro; IPR001774; BSL.
InterPro; IPR00179; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
FIGHER PF01414; DSL; 1.
PF00008; EGF_IC.
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PROSITE; PS00022; EGF_1; 8.
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EMBL, AF030031; AA41249.1; -.
HSSP, P00740; IEDM.
ZFIN; ZDB-GENE-980526-29; dla.
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PROSITE; PSO10186; EGF_2; 8.
PROSITE; PSO1026; EGF_3; 6.
PROSITE; PSO1187; EGF_CA; 1.
EGF-1ike domain.
SEQUENCE 802 AA; 88001 AM
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802 AA; 88941 MW;
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SMART; SM00051; DSL; 1.
SMART; SM00179; EGF CA; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYC 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGRRSALAL-AVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGG---SGPPCACR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
NCBI_TaxIb=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 67.4%; Score 2778; DB 2; Length 7 Best Local Similarity 62.3%; Pred. No. 6.3e-184; Matches 490; Conservative 87; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg K.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075742; AAH75742.1; -.
Hypothetical protein.
SEQUENCE 772 AA; 84968 MW; 716A014158938576 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                      MEDLINE=22388257; PubMed=12477932;
                                                                                   [1]
SEQUENCE FROM N.A.
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Battchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleron M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Frange C.,

RA Basak S.A., McKernan N.J., Abramson R.D., Mullahy S.J.,

RA Basak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Raday J., Helton B.K., Ketreman M., Madan A., Rodrigues S., Sanchez A.,

Rahting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Ratkesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ratkrayinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Tophenski M.I., Skalska U., Smailus D.E., Schmerch A., Schhein J.E.,

R. Monse S.J., Marra M.A.,

R. Monse S.J., Marra M.J.,

R. Monse S.J., Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W. Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO44262; AAH44262.1; -.
HSSP, P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IE.
GO; GO:000154; P:cell communication; IEA
INCEPPO: IPR00152; ABX_hydroxyl_S.
INCEPPO: IPR00174; DSL.
INCEPPO: IPR00174; EGF 2.
INCEPPO: IPR001881; EGF 2.
INCEPPO: IPR001881; EGF 7.
INCEPPO: IPR001881; EGF 7.
INCEPPO: IPR001891; EGF 7.
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MEDLINE=22341132; PubMed=12454917;
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       MEDLINE=22388257; PubMed=12477932
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PERM; PROGOGS; EGF; 5.
PERM; PROGOGS; EGF; 5.
PERMITS; PROGOGS; EGF; 6.
SWART; SWOODS; DSL; 1.
SWART; SWOODS; DSL; 1.
SWART; SWOODS; EGF; 1.
PROSITE; PSOGOGS; EGF_1; 8.
PROSITE; PSOGOGS; EGF_2; 7.
PROSITE; PSOILES; EGF_2; 7.
EGF-1ike domain.
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                                                                                                                                                                                                                         99 TFFRICLKHYQPNASPEPPCTYGGTVTPVLGSNSFQVPDTLP-DGSFTNPIRMNFGFTWP 157
                                                                                                                                                                                                                                                                                                                                                                                                               218 VCDEHYYGEGCSVFCRPRDDAFGHFTCGERGEIICDAGWKGQYCTEPICLPGCDEEHGFC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCDEHYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DKPGECKCRVGWQGRYCDECIRYPGCVHGTCQOPWQCNCQEGWGGLFCNQDLNYCTHHKP 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKCVDLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSAPVSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHM 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQIASDVPWTAVGSGVLLVLLVVACAVVVVCVRSKVQQRRRDREDEVANGENETINNLT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NCOREKDVSVSIIGATQIKNTNKKADFHGDHG-----AEKSSFKVRYPTVDYNLVRDLK 648
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                                                                                                                            39 MGRHLLLLESILYMLLCQASSGVFELKLQEFLNKKGVQGNKNCCKGGLTTSYQQCECK
                                                                                                                                                                                                                                                                                                                     ---SGPPCACR
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MC52561 protein.
Nenopus laevis (African clawed frog).
Renopus laevis Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anvaa; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                    54;
    Length 802;
                                                                                            1 MGRRSALAL-AVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGG
                                                    Indels
65.8%; Score 2713; DB 2;
62.6%; Pred. No. 2.1e-179;
iive 93; Mismatches 135;
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TISSUE=Embryo;
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                                                                                           Gaps
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                                            Length
642 AA; 70655 MW; S6AFB4013E1C2AE2 CRC64;
                                          46.2%; Score 1902; DB 2; ilarity 48.1%; Pred. No. 2.3e-123; Conservative 100; Mismatches 184;
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603
                          YGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPGEC 242
                                   BLSAMTCADGPCFNGGRCSDNPDG-GYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCVD 421
                                                                                                                                           344 DISAMTCEDGPCFNGGTCIEKSSGVGYVCRCPFNYHGSNCEKKIDRCTNSPCLNGGQCLD 403
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718 IATEV 722
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Search completed: November 29, 2004, 13:26:05 Job time : 88.9238 secs

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Aaw00876 C-Delta-1
Aaw11719 C-Delta-1
Aay79029 Chick del
Aay79028 Murine de
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                                                       November 29, 2004, 13:11:34 ; Search time 60.7823 Seconds (without alignments) 3411.281 Million cell updates/sec
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3383
1 MGRLLASALLCVSGVFELKL......DTKYQSVYVSEKDECIATEV 578
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Aab53064
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Aab00172
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                      protein search, using sw model
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AAW75492
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Gapop 10.0 , Gapext 0.5
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geneseqp2003as:*
geneseqp2003bs:*
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ALIGNMENTS

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C-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma; neurogenesis; therapy.
                                                         C-Delta-1 polypeptide (alternatively spliced variant).
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/label= EGF8
524. :54
/label= EGF9
555. :579
/noce= "transmembrane domain"
                                                                                                                   Location/Qualifiers
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             AAW00876 standard; protein; 740
                                                                                                                                                                                                                JGF5
410. .447
/label= EGF6
448. .485
/label= EGF7
/86. .50
                                                                                                                             184. .228
/label= DSL
229. .261
/label= EGF1
262. .292
/label= EGF2
                                                                                                                                                                       293. 332
/label= EGF3
333. 370
/label= EGF4
371. 409
/label= EGF5
410. .447
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                                          (first entry)
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                                          28-APR-1997
                                                                                                      Gallus sp
                            AAW00876;
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Domain
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611 SISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAK 670
--SSIGATQIKNTNKK-DFH----DK---KVRYP-VDYNLVLKV------HKKC--- 541
                                                                             :|||:
671 CETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vertebrate Delta protein, DNA and antibodies - for treating and preventing cancer, nervous system disorders and for tissue regeneration.
                                                                                                                                                                                                                                                                                                     C-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung cancer; colon cancer; melanoma; seminoma; neurogenesis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-delta-1 polypeptide (AAW11719) is the chick homologue of Drosophila
                                                               -----SEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV
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                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= EGF4
371. 409
/label= EGF5
410. 447
/label= EGF6
448. 485
/label= EGF7
                                                                                                                                                                                                                                                                                                                                                                                                                                                229. .261
/label= EGF1
262. .292
/label= EGF2
293. .332
/label= EGF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      // 1254. .534
/label= EGF9
555. .579
/label= TM
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label= EGF8
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                                                                                                                                                                            AAW11719 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                    84. .228
label= DSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333. .370
/label= EG
                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                         C-Delta-1 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-1995;
                                                                                                                                                                                                                                        28-APR-1997
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   505
                                                                                                                                                                                                            AAW11719;
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                                                                                                                                                                                                                                                                                                                                                                    Gallus
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                                                                                                                                                               AAW11719
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                                                                                                                                                                                         C-delta-1 polypeptide (AAW00876) is the chick homologue of Drosophila Delta, a protein that binds to Notch protein. Expression of C-Delta-1 correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (AAT58898) obtd. from chick stage 4-6 embryos. A shorter version (AAM58877) of C-Delta-1, lacking the 12 C-terminal amino acids of the longer version, was also isolated, and mouse (AAW11720) and human (AAW11721-38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders or colon cancer, melanoma or seminoma, and nervous system disorders promote tissue regeneration and repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDKPGEC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCRVGWOGRYCDECIRYPGCLHGTCQOPWOCNCQEGWGGLFCNQDLNYCTHHKPCKNGAT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAOCVDL 430
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                                                                                                                                                           New vertebrate Delta protein, DNA and antibodies - for treating and preventing cancer, nervous system disorders and for tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Indels 144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 740;
                                                                  Artavanis-Tsakonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LASALLC-----VSGVFELKLQEFVNKKGLL-NRNCCRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2489; DB 2;
Pred. No. 2.9e-113;
9; Mismatches 19;
                                                                Lewis J,
             (IMCR ) IMPERIAL CANCER RES TECHNOLOGY (UYYA ) UNIV YALE.
                                                                                                                                                                                                          Disclosure; Fig 2; 135pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.6%;
                                                                Ish-Horowicz D, Henrique D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.0
Matches 546; Conservative
                                                                                                             WPI; 1997-100159/09.
N-PSDB; AAT58898.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 740 AA;
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Chick delta protein amino acid sequence.

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KHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLI 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGPVIVDFTEKYTEGQNSQ 550
             correlates with onset of neurogenesis. The C-delta-1 amino acid sequence was deduced from a cDNA clone (AAT58897) obtd. from chick stage 4-6 and subcratively spliced variant (AAW00876) was also isolated, and mouse (AAW1172) and human (AAW11721 - 38) Delta-1 polypeptides have been identified. Delta-1 proteins can be used to treat or prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, and nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV------DEEQ 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 611 ISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAKC 670
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11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQCDCKTFFRVCL
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Delta, a protein that binds to Notch protein. Expression of C-Delta-1
                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                 73.5%; Score 2485.5; DB 2; Length 727; 76.0%; Pred. No. 4.2e-113; ive 10; Mismatches 19; Indels 143;
                                                                                                                                           disorders or to promote tissue regeneration and repair
                                                                                                                                                                                                                                                                                       5 LASALLC----VSGVFELKLQEFVNKKGLL-NRNCCRGGG
                                                                                                                                                                                                            Query Match
Best Local Similarity 76.0°
Matches 545; Conservative
                                                                                                                                                                               Sequence 727 AA;
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This Bequence represents the chart apporer and actor sequence.

This bequence represents the chart contains a sequence which is cleaved by the metalloprotease-disintigrin Kuzbanian (Kuz). Cleavage by Kuz results in two fragments, a soluble amino terminal fragment consisting cessentially of the extracellular domain, and a membrane bound fragment consisting of the transmembrane domain and the intracellular domain. The soluble fragment is able to bind to North. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention relates to the delta cleavage peptides (the activation. Delta cleavage peptides) and chimeric proteins are useful for modulating the activity of motelia card or its antibody, the activity or levels of delta protein or nucleic acid or its antibody, the activity or levels of delta protein is modulated and vice versa. A delta cleavage peptide or its darivative concelled and vice versa. A delta cleavage peptide or its darivative concelled and vice versa. A delta cleavage peptide or its darivative concelled and vice versa. A delta cleavage peptide or its darivative concerning and its antibody, the activity or levels of delta protein is modulated and vice versa. A delta cleavage peptide or its darivative concerning cartivity comparable of binding kuz protein is useful for treating or preventing central nervous system disorders associated with increased levels of delta protein bind kuz protein. A complex of delta protein and kuz protein. A complex of delta protein and seample to bind kuz protein. A complex of delta protein and seample to bind kuz protein. A complex of delta protein and sample to bind kuz protein. A complex of delta protein and seample to bind kuz protein. A complex of complex, comprising measuring the ability of delta protein and seample to bind kuz protein. A complex of complex or RNA encoding delta or kuz in a sample. The delta cleavage confise. Keloid formation protein protein protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New cleavage peptide, nucleic acids and antibodies useful for diagnosis, prevention and treatment of cancer, disorders of central nervous system,
                                      Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer; lung; melanoma; seminoma; central nervous system disorder; psoriasis; tissue regeneration; liver cirrhosis; keloid formation; baldness; inner ear disorder; chick.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LASALLC-----GCCTFFRVCLL-NRNCCRGG------GCCTFFRVCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence represents the chick delta protein amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2483; DB 3;
Pred. No. 5.6e-113;
9; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                              Η;
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98US-0104834P.
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llarity 75.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Artavanis-Tsakonas S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-282852/24.
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nes 545; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       (UYYA ) UNIV YALE.
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65

Indels 144; Gaps

Length 728;

70

LISALLCRCQVDCSGVFELKLQEFVNKKGLLSNRNCCRGGCPGGAGQGQCDCKTFFRVCL

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06-JUN-2000 (first entry)

AAY79029;

AAY79029 ID AAY7 XX AC AAY7 XX DT 06-J

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Rand

Artavanis-Tsakonas S,

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71 KHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLI 130
                                                         131 IEALHTDSPDDLTTENPERLISRLATORHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHY 190
                                                                                                     YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC 211
                                                                                                                     KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT 270
                                                                                                                                                                                CINTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
                                                                                                                                                                                                                                            CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNC 370
                                                                                                                                                                                                                                                                                       ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
                                                                                                                                                                                                                                                                                                              371 BLSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDL 430
                                                                                                                                                                                                                                                                                                                                                      GNSY-C-CQAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Delta, Kuz, Notch, differentiation; cervical; breast, colon; cancer; lung; melanoma; seminoma; central nervous system disorder; psoriasis; tissue regeneration; liver cirrhosis; keloid formation; baldness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine delta protein amino acid sequence.
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98US-0092513P. 98US-0104834P. 99WO-US015817 (UYYA) UNIV YALE. WO200002897-A2. 13-JUL-1999; 19-OCT-1998; 20-JAN-2000

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This sequence represents the murine delta protein amino acid sequence.

Delta is a toporythmic protein that contains a sequence which is cleaved

by the metalloprotease-disintigrin Kuzbanian in Kuzb. (Leavage by Kuz

results in two fragments, a soluble amino terminal fragment consisting

cresults in two fragments, a soluble amino terminal fragment consisting

cresults in two fragments domain, and a membrane bound fragment

consisting of the transmembrane domain and the intracellular domain. The

consisting of the transmembrane domain and the intracellular domain. The

coluble fragment is able to bind to Notch. Delta plays a key role in

differentiation, and therefore detection and measurement of delta

cortivation is important in the study of differentiation. The invention

cortivation is important in the study of differentiation. The invention

cortivate of the delta cleavage peptides (the activation Delta cleavage

peptides, and chimmeric proteins are useful for modulating the activity of

methods for detecting and measuring delta activation. Delta cleavage

cortivation and proteins are useful for modulating the activity of

corpable of binding kuz protein is useful for treating or preventing a

disease or disorder associated with increased delta activity or

cuseful for treating or preventing central nervous system disorders. A

cuseful for treating or preventing central nervous system disorders. A

cuseful for treating or preventing central nervous system disorders associated with increased levels of delta cleavage peptides in a

custivity comprising measuring the ability of delta cleavage peptides in a

custivity comprising measuring the ability of delta cleavage peptides in a

corplex, comprising measuring the ability of delta cleavage peptides is useful for the diagnosis of delta cleavage peptide is useful for the presence of, or predisposition to

complex, comprising measuring the ability of delta cleavage peptide is also useful for promoting dispense or disorder associated with aberrant levels of creat
                                                                                                                               and antibodies useful for diagnosis, disorders of central nervous system,
                                                                                                                               peptide, nucleic acids nd treatment of cancer,
                                                                                                                                                                                                                                        Claim 1; Fig 3; 177pp; English
                                                                                                                                                                                   cirrhosis and psoriasis.
                                                                             WPI; 2000-282852/24.
                                                                                                                                                          prevention and
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Sequence 722 AA;

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                                                                                                                       VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS 100
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                                                                                                                                                                               LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDE 156
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                                                                             1 MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG-----GCCTFFR
 Score 2467; DB 3; Length 722;
Pred. No. 3.3e-112;
6; Mismatches 19; Indels 144; Gaps
72.9%;
76.6%;
                                  Matches 553; Conservative
                    Similarity
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    Query Match
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or

can be used to treat

Delta-1 proteins

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also been identified.
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Matches 553;
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ATCINTGQGSYTCSCRPGYTGANCELEVDECDPSPCKNGASCTDLEQSFSCTCPPGFYGK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and antibodies - for treating and disorders and for tissue regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M-delta-1 polypeptide (AAW11720) is the mouse homologue of Drosophila Delta, a protein that binds to Notch protein. It is expressed primarily in presomitic mesoderm, the central and peripheral nervous systems, and kidney. Chick (AAW11719) and human (AAW11721- 38) Delta-1 polypeptides
             DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P
                                                                                                                 GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMNNLANCQREK
                                                                                                                                        D---SSIGATQIKNTNKK-DFHDK------KVRYP-VDYNLV--LK------VHKK
                                                                                                                                                cancer;
                                                                                                                                                                      ------CSEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT
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                                                                                                                                                                                                                                                                                                                     M-Delta-1; cell proliferation; nervous system disorder; tissue regeneration; Notch; cervix cancer; breast cancer; lung colon cancer; melanoma; seminoma; neurogenesis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lewis J, Artavanis-Tsakonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New vertebrate Delta protein, DNA preventing cancer, nervous system
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Gray GE;
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prevent disorders characterised by increased Notch activity, such as cervical, breast, lung or colon cancer, melanoma or seminoma, as well as nervous system disorders, and to promote tissue regeneration and repair
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                                                                                                                                                   Gaps
                                                                                                                                                   144;
                                                                                                             Length 722;
                                                                                                                                                   Indels
                                                                                                             72.9%; Score 2466; DB 2; llarity 76.6%; Pred. No. 3.7e-112; Conservative 6; Mismatches 19;
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Φ

Sequence 722 AA;

ligand; Parkinson's disease; Huntington's disease; motor neuron disease; heart disease; diabetes; liver disease; cirrhosis; renal disease; AIDS; acquired immunodeficiency syndrome.

Mus sp

WO200277204-A2

03-OCT-2002

25-MAR-2002; 2002WO-GB001195

23-MAR-2001; 2001GB-00007296. 23-MAR-2001; 2001GB-00007299. 17-APR-2001; 2001GB-00009346.

(AXOR-) AXORDIA LTD

Gokhale Andrews P, Walsh J,

WPI; 2003-092852/08

N-PSDB; ABX75296

Modulating the differentiation of embryonic stem cells by providing ligands which bind receptors in the Notch and Wnt pathways, useful for treating diseases such as Parkinson's, Huntington's, heart disease, diabetes and AIDS.

Claim 6; Fig 3; 121pp; English.

The invention relates to modulating the differentiation of an embryonic stem cells.

Stranged to comprising: (a) providing a culture of embryonic stem cells.

(b) providing at least one ligand or its active binding fragment, capable of binding its cognate receptor polypeptide expressed by the embryonic stem cells.

(c) binding its cognate receptor polypeptide expressed by the embryonic stem cells.

(d) forwing a culture comprising embryonic stem cells.

(e) forwing a culture comprising embryonic stem cells.

(i) any of § fully defined with an uncleic acid molecule selected from: comprising a cell transfected with a nucleic acid sequences.

(i) any of § fully defined with uncleic acid sequences; (ii) a nucleic acid molecule that hybridies to the nucleic acid in (i), and which endocase a ligand capable of binding a whit receptor; or (iii) nucleic acid molecules which are degenerate as a result of the genetic code to the sequences of (i) or (ii); (b) forming a culture comprising the cell identified in (a) with an embryonic stem cells, and (a) growing the cell culture for the maintenance and/or differentiation of the embryonic stem cells (a) providing at least one polypeptide or its active cell; (a) Inhibition the differentiation of embryonic stem cells in an undifferentiated state; or (i) Inhibiting the differentiation of embryonic stem cells in an undifferentiated state; or (i) Inhibiting the differentiation of embryonic stem cells in an undifferentiated state; or (i) Inhibiting the differentiation of embryonic stem cells in an undifferentiated state; or (i) Inhibiting the differentiation of embryonic stem cells in an undifferentiated state; or (i) inhibiting put coll coll capable of thinhibiting which signalling a culture for the maintenance of corpusation of embryonic stem cells in an undifferentiated state; or (i) inhibiting which signalling a culture for the maintenance of comprising a coll dendicial selected from (i) with an uncleic acid molecule selected from (i) inhibiting by propering the cell identified

100 61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120 156 180 209 240 300 360 367 9 540 9 576 317 420 415 480 503 45 9 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG ATCINTGOGSYTCSCRPGYTG--CE---BEC---PCKNG-SCIDLES--SCTCPPGFYGK D---SSIGATQIKNTNKK-DFHDK------KVRYP-VDYNLV--LK------VHKK -----CSEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG -CELSAMICADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDE DIGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNLANCQREK VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ-Gape 144; screening; toxicology assay; signalling pathway; delta-like 1. Length 722; 19; Indels 1 MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG Score 2466; DB 6; Pred. No. 3.7e-112; 6; Mismatches ligand delta-like 1 protein. AAE34029 standard; protein; 722 AA 72.9%; (first entry) Conservative Similarity EV 578 Murine; drug notch ligand notch 553; 02-MAY-2003 н 46 121 269 301 318 421 601 157 181 210 241 368 416 504 541 Query Match Local Matches à 셤 ద ò 셤 ò 요 ઠે 원 ò 셤 ò 셤 õ 유 ò ద ò g ò 셤 ò 요 ò

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361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proliferation; differentiation; suppression; human; delta-1; serrate-1; blood cell; neuron; leukaemia; malignant tumour; immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a polypeptide which suppresses proliferation and differentiation of undifferentiated cells such as neurons and blood cells. The polypeptide may be used for the prevention and control of disorders involving undifferentiated cells, such as
                                     GPFPWVAVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPFPCGGETETWNNLANCQREK
                                                                                                                                                                                                                                                                                                                                                        --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK
                                                                                                                                                                                                                                                               D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV--LK-----VHKK
                                                                                                                                                                                                                                                                                      VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ-
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/label= Signal
22. .723
/label= Differentiation_suppression_protein
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                                                                                                                                                                                                                                                                                                                 Identifying biologically active agents comprises cloning transfected cells into a cell array, exposing the array to an agent to be tested, and detecting signals generated by a reporter molecule as a result of exposure to the agent.
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                                                                                                                                                                                                                          Walsh J;
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Fig 2; 90pp; English.
                                                                                                             29-APR-2002; 2002WO-GB001946
                                                                                                                                                  04-MAY-2001; 2001GB-00011004
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N-PSDB; AAD52523.
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/note= "mature delta-1 protein" "signal peptide"

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'note=

Location/Qualifiers

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This sequence represents the human delta-1 protein, which is a ligand of the human notch protein. The protein or fragments, especially AAW75493-W75495, can be used as a drug to control vascular cells. The sequences were isolated and the truncated fragments were generated using the
                                                                                                                                                                                            Disclosure; Page 16-19; 21pp; Japanese
                                                                                                                                                                  Vascular cell controlling agent c
notch ligand and is used as drug.
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N-PSDB; AAX16817.
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11; Mismatches 27; Indels
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                                                                            TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD
                                                                                                                                                                                                                                                                                                                                                                                         TCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCAD
                                                                                                                                                                                                                                                                                                                                                                                                                                       GPCFNGGRCSDSPDGGSCRCPVGSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VL---LLLGCAA-VVCVRL---KQKPEC----ETETMNNLANCQREKD---SSIGATQI
                                                                                                                      PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP
                                                                                                                                                                                                                                         RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR
                                                                                                                                                                                                                                                         RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR
                                                                                                                                                                                                                                                                                                 YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY
                                                                                                                                                                                                                                                                                                                    YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY
                                                                                                                                                                                                                                                                                                                                                                                                                        GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ
                                                           SALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG-----GCCTFFRVCLKHYQASVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCHRR----YCECA-GYGG-NCOFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL
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                               139;
   Length
                               IndelB
71.0%; Score 2401.5; DB 2; 75.1%; Pred. No. 5e-109; ive 11; Mismatches 27;
                               Conservative
                               534;
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cell; primer;

drug; vascular

notch;

protein; ligand;

Human; delta-1 amplification.

sapiens

Homo

Human delta-1 protein

27-APR-1999

AAW75492

167

279

312

220 252 327 372 376 425 492 467 552 512 612 542

432

672

40. .46 /note= "N-myristoylation site" 93. .97

Addified-site Modified-site

--- GCCTFFRVCLKHYQASVS 56

SALLC --- VSGVFELKLQEFVNKKGLL - NRNCCRGG-

8

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SALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGAGPPCACRTFFRVCLKHYQASVS 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; PRO211; PRO228; PRO538; PRO172; PRO182; human.
                                                                    280 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD
                                                                                                                                                                                                                                                                                                                                                                                                     TCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATCHRR----YCECA-GYGG-NCQFLLPB-PPGP--VD-----BDQ---FPW-AVCAGL
                                               PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRPPFGFTWPGTFSLIIEALHTDSP
                                                                                                                                                                                                                                                      193 RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR
                                                                                                                                                                                                                                                                                              YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613 KNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSG
                                                                                                                              DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC
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    .8
    note= "N-myristoylation site"

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    .21
    label= Signal peptide

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                                                                  542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes full length and shortened human delta-2 proteins. Human delta-2 is a differentiation inhibitor which inhibits the differentiation of undifferentiated cells (other than brain or muscle cells), such as blood cells, and enhances the proliferation of undifferentiated blood cells. Products of human delta-2 may be used for the treatment of diseases such as leukaemia and malignant tumours. They may also be used in the culture of human cells in vitro, e.g. for production of supplies of undifferentiated blood cells. The present sequence represents human delta-1, from an example of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentiation inhibitor; proliferation;
                                                                                                                                               BEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
                                                                                                                                                                         KNTNKK-DFH-----DK---KVRYP-VDYNLV-----
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/label= Delta-1
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/label= signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; delta-1; delta-2; dif
leukaemia; malignant tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                  Human delta-1 protein.
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e= "Casein kinase II phosphorylation"
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label= Asn and Asp hydroxylation site
(57. .479
label= EGF-like_domain
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/note= "N-myristoylation domain"
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82. .288
                                                                                                                                                                                                                                        /note= "N-myristoylation site"
310. .316
/note= "N-myristoylation site"
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'note= "N-myristoylation site"
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/label= Transmembrane_domain
                                                                                                                                                                            174. .286
'note= "EGF-like domain"
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/label= EGF-like_domain
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/label= EGF-like_domain
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|abel= EGF-like_domain
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/label= EGF-like_domain
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42
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/note= "N
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|abel= F
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262. .268
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378. .384
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67;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition for inhibiting neoplastic cell growth and treating cancers of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279
         'label= Prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLPCNQDLNYCTHHKPC-NGATCTNTGQGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 SALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG-----GCCTFFRVCLKHYQASVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR
                                                                                                                                                                                                                                                                                                                                                               Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%; Score 2401.5; DB 3; Length 723; 75.1%; Pred. No. 5e-109; ive 11; Mismatches 27; Indels 139;
                                                                 dependent protein kinase
                                                                                                     "Casein kinase II phosphorylation site"
                                                                                                                            "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                      'note= "Casein kinase II phosphorylation site"
                                           "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                               Napier M,
                                                                                                                                                                                                                                                                                                                                                               Klein RD,
                                                                                                                                                   "N-myristoylation site"
                                                                                                                                                                        /note= "N-myristoylation site"
                                                                                                                                                                                                /note= "N-myristoylation site"
598. .702
                                                                   "CAMP and CGMP
                                                                              phosphorylation site"
670. .674
/note= "Casein kinase
                                                                                                                                                                                                                                                                                                                                                                Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Fig 8; 122pp; English.
                                                                                                                                                                                                                                                                                                                 98US-0104080P.
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/note= "Car
676.
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                                .663
                                                      .664
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                                                                                                                                                   'note=
                                              'note=
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                            AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425
                                                                                                     AGPSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHN 492
                                                                                                                           GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD----EEQ---FPW-AVCAGL 467
                                                                                                                                              552
                                                                                                                                                               VL---LLLGCAA-VVCVRL---KQKPEC----ETETMNNLANCQREKD---SSIGATQI 512
                                                                                                                                                                           KNTNKK-DFH-----DK---KVRYP-VDYNLV-------LKVHKKC-----S 542
                                                                                                                                                                                                               253 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312
                                                                                                                                                                                                                                                                                                                                                                         Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antithryoid; antidabbetic; noctropic; neuroprocective; antiansemic; hepatoropic; virucide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; didopathic inflammatory myopathy; Sjogren's syntrome; thyroiditis; systemic vasculitis; autoimmune hemolytic ansemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; autoimmune disease; hepatobliary disease; Mhipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; ilmmune-mediated skin disease; allergic disease; ranaplantation associated disease;
                  TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD
                                                    GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ
                                                                                                                                      EEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
                                                                                                                                                                                                                                                  graft rejection; graft-versus-host-disease
                                                                                                                                                                                                                                                                                                                                                           Human PRO172 protein UNQ146 SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                      AAB33422 standard; protein; 723 AA
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99US-0123957P.
99US-0123957P.
99US-0125849P.
99WS-0131445P.
99US-013145P.
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28-APR-1999;
04-MAY-1999;
14-MAY-1999;
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12-MAR-1999;
23-MAR-1999;
12-APR-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and disquosing immune related disorders are useful for treating and disquosing immune related disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthitis, juvenile chronic arthritis, spondyloarthogathiss, systemic sclerosis, idiopathic inflammatory myopathies, Sjogran's systemic vasculitis, saxcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune diseases, altergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58337 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO polymucleotide and protein sequences given in the represent human PRO polymucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Pan J, Pennica D, Shelton DL, Smith V;
Watanabe CK, Wood WI, Yan M;
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99US-0141037P.
99US-0144758P.
99US-0145698P.
99US-0146222P.
99WO-US020111.
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2000WO-US003565.
2000WO-US004341.
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99US-0162506P
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2000WO-US000277
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Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-572271/53.
N-PSDB; AAC58587.
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Kabakoff RC, Lu
Stewart TA, Tur
                                                                                                            01-SEP-1999;
08-SEP-1999;
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11-FEB-2000;
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11-DEC-1999
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16-DEC-1999
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7 SALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG-----GCCTFFRVCLKHYQASVS 56

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PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP 111
                                                              132
                                                                                      DDL-TENPERLISRL-TORHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC 167
                                                                                                          DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDEHYYGEGCSVFC 192
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                                                                                                                                                                                              253 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY 312
                                                                                                                                                                                                                                  TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
                                                                                                                                                                                                                                               TCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCAD 372
                                                                                                                                                                                                                                                                                 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376
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               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSG
RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR
                                                                                                                                                           RPRDDAFGHFTCGERGEKVCNPGWKGPYCTEPICLPGCDEQHGFCDKPGECKCRVGWQGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; vaccine
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98US-0112850P
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16-DEC-1998;
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The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy.) For example, the nucleic acids (NCS) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB24415 represent nucleocide and protein sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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Paoni NF;
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                                                                                                                                                                                                                                                                            Hillan K
Kuo SS,
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Klein RD,
Wood WI;
                                                                                                                                                                                                                                                                          , Ferrara N,
, Gurney AL,
Williams PM,
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99US-0115554P.
99WG-US005028
99US-0131445P.
99UG-0131287P.
99UG-0141037P.
99UG-0141037P.
99UG-0145698P.
99WG-US020594.
99WG-US020594.
99WG-US020594.
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                                                                                                                                                                                                                                                                            Baker KP,
lowski PJ,
                                                                                                                                                                                                                                                                                                         Watanabe CK,
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                                                                                                                                                                                                                                                                                             Godowski
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N-PSDB; AAA77512.
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12 JAN-1999,
08-MAR-1999,
12-MAR-1999,
14-MAY-1999,
02-JUN-1999,
20-JUL-1999,
20-JUL-1999,
01-SEP-1999,
01-SEP-1999,
13-SEP-1999,
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05-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                                                                                                         Smith V,
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                                                                                                                                   TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD
                              GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ
                                                                                                                                                                                                             AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN
                                                                                                                                                                                                                                                            AGFSGRHCDDNVDDCASSPCANGGTCRDGVNDFSCTCPPGYTGRNCSAPVSRCEHAPCHN
                                                                                                                                                                                                                                                                                                                     GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL
                                                                                                                                                                                                                                                                                                                                                                    GATCHERGHRYVCECARGYGGPNCOFLLPELPPGPAVVDLTEKLEGGGGPFPWVAVCAGV
                                                                                                                                                                                                                                                                                                                                                                                                                        VL---LLLGCAA-VVCVRL---KQKPEC----ETETMNNLANCQREKD---SSIGATQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KNTINKK-DFH-----DK---KVRYP-VDYNLV-------LKVHKKC----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung; melanoma; seminoma; central nervous system disorder; psoriasis;
tissue regeneration; liver cirrhosis; keloid formation; baldness;
inner ear disorder; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta; Kuz; Notch; differentiation; cervical; breast; colon; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578
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N-PSDB; AAZ98679.
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consisting of the transmembrane domain and the intracellular domain. The soluble fragment is able to bind to Notch. Delta plays a key role in differentiation, and therefore detection and measurement of delta activation is important in the study of differentiation. The invention carrivation is important in the study of differentiation. The invention content of the delta cleavage peptides (the active fragment), and to content of the delta or the delta activation. Delta cleavage peptides, and chimeric proteins are useful for modulating the activity of Notch, delta or kuz or at least one of the signalling pathways in a cell content or the supportance of the signalling pathways in a cell content or transmism, expressing Notch. By contacting a cell with kuz protein or nucleic acid or its antibody, the activity or levels of delta protein is modulated and vice versa. A delta cleavage peptide or its derivative capable of binding kuz protein is useful for treating or preventing and classase or disorder associated with increased delta activity or seminoma in humans. A recombinant cell comprising a delta peptide is useful for the diagnosis of diseases or certificated with increased levels of Notch-delta protein binding contents or preventing central nervous system disporters. A cells caleavage peptide is useful for the diagnosis of diseases or continuous protein. A complex of delta protein and kuz is useful. Content of containing the ability of delta cleavage peptide is useful for the diagnosis of diseases or contained with increased levels of forth and kuz is useful.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 GPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complex, comprising measuring the level or functional activity of the complex or RNA encoding delta or kuz in a sample. The delta cleavage peptide is also useful for promoting tissue regeneration and repair, fracting liver cirrhosis, keloid formation, psoriasis, baldness and degenerative or traumatic disorders of the sensory epithelium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDEHYYGEGCSVFC
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Best Local Similarity
Matches 534; Conserv
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This sequence represents the human delta protein amino acid sequence. Delta is a toporythmic protein that contains a sequence which is cleaved by the metalloprotease-disintigrin Kuzbanian (Kuz). Cleavage by Kuz results in two fragments, a soluble amino terminal fragment consisting essentially of the extracellular domain, and a membrane bound fragment

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"EGF-like domain cysteine pattern signatu"
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/note= "Casein kinase II phosphorylation site"
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note= "Asx hydroxylation site"
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note= "Asx hydroxylation site"
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"N-myristoylation site"
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.441
/label= FC
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.59.
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05-OCT-1999;
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                     --LKVHKKC----S 542
                                        613 KNTNKKADFHGDHSADKNGFKARYPAVDYNLVQDLKGDDTAVRDAHSKRDTKCQPQGSSG 672
                                                                                                                                                                                                                        PRO211; PRO228; PRO538; PRO172; PRO182; neoplasia; inhibition; tumour; treatment; therapy; agonist; antibody; breast cancer; ovarian cancer; renal cancer; uterine cancer; prostate cancer; lung cancer; prostate cancer; analanoma; leukaemia; inflammatory disorder; angiogenic disorder; immunologic disorder; human.
                                                              543 EEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
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|EKGTPTTLRGGEASERKRPDSGCSTSKDTKYQSVYVISEEKDECVIATEV 723
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note= "Tyrosine kinase phosphorylation site"
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/label= Signal peptide
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Isolated PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptides or their agonists (preferably anti-PRO agonist antibody or a small molecule amincking the biological activity of PRO polypeptide) are useful in vitro or in vivo for inhibiting the growth of a tumour cell. Compositions comprising the PRO polypeptides are useful for inhibiting neoplastic cell growth and for treating cancer including breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, central nervous system cancer, melanoma and leukaemia in a mammal. The PRO polypeptides are also useful for treating other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal, blastoccellc disorders and inflammatory, angiogenic and immunologic disorders as well as being useful for identifying agonists to PRO polypeptides by contacting the polypeptide with a candidate molecule and monitoring biological activity mediated by the polypeptide
                                                                                                                                                                                 PRO211, PRO228, PRO538, PRO172 and PRO182 polypeptides useful for treating tumors including cancers of the breast and lung, leukemia and for identifying compounds capable of inhibiting growth of neoplastic cells.
                                                                     Wood WI;
                                                                   Ashkenazi AJ, Goddard A, Gurney AL, Klein RD, Napier MA,
                                                                                                                                                                                                                                                                                                                       Claim 31; Fig 8; 133pp; English.
                     (GETH ) GENENTECH INC
                                                                                                                                   WPI; 2000-638201/61
                                                                                                                                                           N-PSDB; AAA54105
                                                                                             Yuan J;
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Query Match 71.0%; Score 2401.5; DB 3; Length 723; Best Local Similarity 75.1%; Pred. No. 5e-109; Matches 534; Conservative 11; Mismatches 27; Indels 139; Gaps

Sequence 723 AA;

PEPPCTYGSAVTPVLGVDSFSLPDGGGADSAFSNPIRFPFGFTWPGTFSLIIEALHTDSP 132 PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP 111 DDL-TENPERLISRL-TORHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC 167 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR 220 YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY 279 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQSSY 312 GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376 GPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432 AGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRCEH-PCHN 425 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327 GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD----EEQ---FPW-AVCAGL 467 13 133 221 57 73 112 168 193 253 280 313 328 373 377 433 426 a 8 ઠે 유 ò 셤 8 6 ઠે g ò ያ ያ ò g ઠે δ

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468	553	513	613	543	673	
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(c) 1993 - 2004 Compugen Ltd
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US-09-908-322-12

US-09-908-322-12

US-09-423-753-27

US-09-423-753-27

US-09-641-612-6

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100.0%; Pred. No. 3.3e-245;
Ative 0; Mismatches 0;
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                   NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMUNICATION INFORMATION:
TELEFYX: 212-790-9090
TELEFX: 212-869-864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ 1D NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                             LENGTH: 578 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 100.
578; Conservative
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TITLE OF INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                              MGRLLASALLCVSGVFELKLQEFVNKKGLLNRNCCRGGGCCTFFRVCLKHYQASVSPEPP
                                                                                                       CTYGSATPVLGSFSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDDLTENPER
                                                                                                                                                                                                                                                                                                                                                    GEKCPGWKGQYCTPICLPGCDQHGCDKPGECKCRVGWQGRYCDECIRYPGCVHGTCQQPW
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  MGRLLASALLCVSGVFELKLQEFVNKKGLLNRNCCRGGGCCTFFRVCLKHYQASVSPEPP
                                                                                                                                                                                                                 LISRLTORHLVGEEWSODLHSSGRTDLYSYRFVCDEHYYGEGCSVFCRPRDDFGHFTCGR
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Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: IBH-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OMPUTER: IBM Compatible
OURRENT APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-U1-2001
PRIOR APPLICATION NUMBER: US/09/908, 322
FILING DATE: 22-DEC-1997
FILING DATE: 22-DEC-1997
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STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
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CORRESPONDENCE ADDRESS:
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505 --SSIGATQIKNTNKK-DFH----DK---KVRYP-VDYNLVLKV-------HKKC--- 541
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                                                                                                                                                                                                                                                                                                                                                                     542 -----SEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
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671 CETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
                                                                                                              FPW-AVCAGLVL---LLLGCAA-VVCVRLK----QKPEC---ETETMNNLANCQREKD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
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ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/09908322; Patent No. 6783956; GENERAL INFORMATION:
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TELEFAX: 212-869-8864
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LENGTH: 728 amino acids
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INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
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      NUCLEOTIDE AND PROTEIN SEQUENCES
OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 2489; DB 3; 76.0%; Pred. No. 3.4e-178; ive 9; Mismatches 19;
TITLE OF INVENTION: NUCLECTIDE AND PROTE
TITLE OF INVENTION: OF VERTEBRATE DELTA
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FOALS.

MEDIUM TYPE: Diskette
COMPUTER: DESCRIPE
SOFTWARE: FESTSED VETSION 2.0
SOFTWARE: FESTSED VETSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ANLIET, Adriane M.
REGISTRATION NUMBER: 32,605
REPERBUCE/DOCKET NUMBER: 7326-038
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEFAX: 212-869-8864
TELEFAX: 6141 PENNIE
INFORMATION: FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TUNDER CHARACTERISTICS:
LENGTH: 728 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 76.0
Matches 546; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: unknown // MOLECULE TYPE: protein US-08-981-392-2
                                                                                                                                                                                                                                                                                     ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS
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RESULT 6
US-08-981-392-12
; Sequence 12, Application US/08981392
; Patent No. 6262025
; GENERAL INFORMATION:
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71 KHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLI 130
                                       158
                                                     131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHY 190
                                                                                         YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC 211
                                                                                                                    250
                                                                                                                                              KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT 270
                                                                                                                                                              KCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGAT 310
                                                                                                                                                                                                 CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
                                                                                                                                                                                                                          311 CINTGOGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNC 370
                                                                                                                                                                                                                                                     ELSAMICADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
                                                                                                                                                                                                                                                                            ELSAMICADGPCFNGGRCIDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDL 430
                                                                                                                                                                                                                                                                                                          GNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417
                                                                                                                                                                                                                                                                                                                                    431 GNSYICQCQAGFIGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVS 490
                                                                                                                                                                                                                                                                                                                                                               RCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV------DEEQ 458
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671 CETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
                                                                                                         YGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDKPGEC
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Patent No. 6121045

Patent No. 6121045

GENERAL INFORMATION:

APPLICANT: Gearing, David

TITLE OF INVENTION: THERAPEUTIC USES THEREFOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OMPUTER: BRADABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: BM PC Compatible

OMPUTER: BM PC Compatible

OMPUTER: BM PC Compatible

OMPUTER: BAPLICATION DATA:

ATPLING DATE: 11-JUN-1997

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
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US-08-872-855-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNC 370
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671 KCETYDSEAEEKSAVOLKSSDTSERKRPDSVYSTSKDTKYOSVYVISEEKDECIIATEV 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 YGEGGSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-OHG-CDKPGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQBGWGGLFCNQDLNYCTHHKPC-NGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHY
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 145;
                                                                                                                                                                                                                                                                                                                                                                 Length 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 LASALLC ---- VSGVFELKLQEFVNKKGLL - NRNCCRGGG
                                                                                                                                                                                                                                                                                                                                                               Query Match 73.6%; Score 2488.5; DB 3; Best Local Similarity 75.9%; Pred. No. 3.7e-178; Matches 546; Conservative 9; Mismatches 19;
REGISTRATION UNDER: 35,430
REGISTRATION UNDER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELECOMMUNICATION INFORMATION:
TELEPHAN: 617-832-1000
TELEPAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
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536

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421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480
                                                                                                                                                                                                601 DVSVSIIGATQIKNTNKKADFHGDHGAEKSSFKVRYPTVDYNLVRDLKGDEATVRDTHSK 660
                                                                                                                                                                                                                                                                                                                                                                     661 RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
  368 DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P
                                                                                                                 -- PPW-AVCAGLV---LLLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK
                                                                                                                                                                                                                                                          504 D---SSIGATQIKNTNKK-DFHDK-----KVRYP-VDYNLV-----LK
                                                                                                                                                                                                                                                                                                                                               ------SEKDEC-IAT
                                                                                    416 VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD------BEQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ISh-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRASESQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
PILING DATE: 17-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7326-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 722 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-866-864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-908-322-12; Sequence 12, Application US/09908322; Patent No. 6783956; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                            537 VHKKCSEEKALRKR-
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STATE: NY
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                 APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 3.5e-176;
6; Mismatches 24;
Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7126-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-190-9090
TELEPHONE: 212-196-9864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 722 amino acids
TYPE: amino acid
                                                                                                                                                                                  ISEE: Pennie & Edmonds LLP
1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.9%;
Matches 548; Conservative
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                                                                                                                                                                                                                                                                                           ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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MOLECULE TYPE: protein
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CITY: Nev
STATE: N)
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                COUNTRY: USA

ZIP: 02109-2170

ZIP: 02109-2170

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,855
FILING DATE: 11-JUN-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: ARTOIG, Beth E. REGISTRATION NUMBER: 35,430
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MAA-003.02
TELEFAX: 617-832-1000
TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.5%; Score 2454; DB 3; 76.4%; Pred. No. 1.4e-175; ive 6; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                LENGTH: 720 amino acids
TYPE: amino acid
STRANDEDNESS:
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Matches 551; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                             HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209
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                                                                                                                          537 VHKKCSEEKALRKR-----------PSVYSTSKDTKYQSVYV--SEKDEC-IAT
                                                                                                      1 MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG-----GCCTFFR
                                                                    Gaps
                                                                  24; Indels 144;
                                  Length 722;
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Patent No. 6121045
GENERAL INFORMATION:
APPLICANT: MCCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                  Score 2462; DB 4;
Pred. No. 3.5e-176;
6; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S: FOLEY, HOAG & ELIOT LLP
One Post Office Square
                                  72.8%;
75.9%;
                                  Query Match
Best Local Similarity 75.9
Matches 548; Conservative
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JS-09-908-322-12
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US-08-872-855-4
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301 TCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGGSCTDLEDSYSCTCPPGFYGKV 360
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                                                                                                                                                                                                                                                                                                                 361 CELSAMICADGPCFNGGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCSSSPCSNGAKCVD 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 AGLV---LLLLGCAA-VVCVRLK----QKP--EC--ETETWNNLANCQREKD---SSIGA 509
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                                                                 241 CKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGA
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                                                                                                                                                 TCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-
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Sequence 9, Application US/09068740A

Sequence 9, Application US/09068740A

GENERAL INFORMATION:

APPLICANT: SAKANO, SEIJI

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION UNBER: US/09/068,740A

CURRENT FILING DATE: 1998-06-18

FRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1995-11-17

PRIOR APPLICATION NUMBER: UP 7-311811

PRIOR FILING DATE: 1995-11-17

PRIOR FILING DATE: 1996-11-15

NUMBER OF SEQ ID NOS: 48

SOFTWARE: PALENTIN VET: 2.1

SEQ ID NO 9

LENGTH 123
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                                                                                     ------CSEEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATE
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Pred. No. 4.2e-175;
9; Mismatches 29; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND
TITLE OF INVENTION: THERAPEUTIC USES THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG
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STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTER: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                            , Sequence 5, Application US/08872855; Patent No. 6121045; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.7%;
Matches 540; Conservative
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                                                                                                                                                     253 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY
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APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
APPLICANTON: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C59
CURRENT APPLICATION NUMBER: US/10/140,002
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 346
LENGTH: 723
TYPE: PRT
                 RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR
                                                                                                 TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD
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                                                                                                                                   YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY
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Filvaroff, Ellen
Gao, Wel-Qiang
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
Tumas, Daniel
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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                                                                                                                                                                     TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
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                                                        253 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGAICTNTGQGSY
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                                                                                                   YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY
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                               RPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGECKCRVGWQGR
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; Pred. No. 1.2e-171;
11; Mismatches 27; Indels 139; Gaps
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PATENT NO. 6664098
GENERAL INFORMATION:
APPLICANT: SAKANO, SELJI
TITLE OF INVENTION: NOVEL DIFFERENTIATION INHIBITOR
FILE FEFERENCE: KF-868
CURRENT APPLICATION NUMBER: US/09/423,753
CURRENT FILING DATE: 1999-12-30
PRIOR APPLICATION NUMBER: UF 1999-12-30
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1908-05-13
PRIOR FILING DATE: 1908-05-13
PRIOR FILING DATE: 1908-05-13
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75.1%;
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Best Local Similarity 75.1<sup>3</sup>
Matches 534; Conservative
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; ORGANISM: Homo sapiens
US-09-423-753-27
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LENGTH: 723
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NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
          SOFTWARE: Pat
SEQ ID NO 4
LENGTH: 702
TYPE: PRT
                                                         ; ORGANISM: HO
US-09-068-740A-4
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                                                                                                                      PEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIBALHTDSP 111
                                                                                                                                                                  DDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC 167
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                                                     27; Indels 139;
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APPLICANT: SAKANO, SEIJI
APPLICANT: SAKANO, SEIJI
APPLICANT: ITOH, AKTRA
ITILE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP-8447
CURRENT APPLICATION NUMBER: US/09/068,740A
CURRENT APPLICATION NUMBER: US/09/068,740A
PRIOR APPLICATION NUMBER: US/09/068,740A
PRIOR FILING DATE: 1995-11-17
PRIOR FILING DATE: 1995-11-30
PRIOR FILING DATE: 1995-11-30
PRIOR FILING DATE: 1995-11-15
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                                DB 4;
                               Query Match
71.0%; Score 2401.5; DB 4,
Best Local Similarity 75.1%; Pred. No. 1.2e-171;
Matches 534; Conservative 11; Mismatches 27;
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; ORGANISM: Homo Sapien
US-10-140-002-346
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US-09-068-740A-4
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                                                                                                                        136;
                                                                          Length 702;
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TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
FILE REFERENCE: PPO-1602.002 / 200130.498
CURRENT APPLICATION VMBER: US/09/641,612
CURRENT FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FABELSEQ for Mindows Version 4.0
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                                                                        Query Match 70.6%; Score 2390; DB 3; Best Local Similarity 75.4%; Pred. No. 8.2e-171; Matches 529; Conservative 11; Mismatches 26;
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Sequence 6, Application US/09641612
Patent No. 6703221
GENERAL INFORMATION:
ORGANISM: Homo sapiens
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COUNTRY: NA
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION NUMBER: US/08/981,392
FILING DATE: 22-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: AALIAN: Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-038
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-790-990
TELEFAX: 212-869-8864
INFORMATION FOR SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acids
TYPE: amino acids
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Avenue of the A
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Best Local Similarity 68.77
Matches 489; Conservative
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TOPOLOGY: unknown
MOLECULE TYPE: peptide
                              New York
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APPLICANT: Henrique, Domingos Manuel Pinto
APPLICANT: Lewis, Julian Hart
APPLICANT: Lewis, Julian Hart
APPLICANT: Artavanis-Teakonas, Spyridon
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES
TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                99
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                                                                                                                                                                   SALLCQVWSSGVFELKLQEFVNKKGLLGNPNCCRGGAGPPPCACRTFFRVCLKHYQASVS
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                                                                                                                     Gaps
                                                                                                                  Indels 139;
                                                                                        Length 723;
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                                                                                                                   30;
                                                                                       70.4%; Score 2380.5; DB 4
74.7%; Pred. No. 4.4e-170;
iive 11; Mismatches 30;
                                                                                                                                                SALLC - - - VSGVFELKLQEFVNKKGLL - NRNCCRGG-
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Patent No. 6262025
GENERAL INFORMATION:
                                                                                     Query Match
Best Local Similarity 74.7%
Matches 531; Conservative
 ; SEQ ID NO 6
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-6
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US-08-981-392-5
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52 QASVSPEPPCTYGSA-TPVLGSFS---PDGA-GDPAFSNPIRFPFGFTWPGTFSLIIEAL 106 107 HTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEG 162 464 CAGLVL---LLLGCAA-VVCVRL----KQKPEC---ETETWNNLANCQREKD---SSIG 508 10 LVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSLASLQRCECKTFFRICLKHY CSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCDQHG--CDKPGECKCRV GWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNT 250 GWQGRYCDECIRYPGCLHGTCQQPWQCNCQBGWGGLFCNQDLNYCTHHKPCENGATCTNT GOGSYTCSCRPGYTG -- CE---EEC---PCKN-GSCTDLESS--CTCPPGFYGK-CELSA 310 GQGSYTCSCRPGYTGSNCEIEVNECDANPCKNGGSCSDLENSYTCSCPPGFYGKNCELSA 374 CCQA--GF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVSRCEH 422 -PCHNGATCHRR----YCECA-GYGG-NCOFLLP-EPPGPVD------EEOFPW-AV MTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSS-PC-NGA-CVDLGNSY 4 LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGGG------CCTFFRVCLKHY Gaps 47; Indels 137; Length 721; DB 3; 66.9%; Score 2262.5; DB 3 68.7%; Pred. No. 2.9e-161; iive 39; Mismatches 47;

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309 322 369

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Sequence 13, Appl
Sequence 13, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 8, Appli
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Sequence 4, Appli
Sequence 12, Appl
Sequence 12, Appl
                                                                                                                                                                                (without alignments)
3520.994 Million cell updates/sec
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                                                                                                                                                       November 29, 2004, 13:26:20 ; Search time 58.226 Seconds
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3383
1 MGRLLASALLCVSGVFELKL......DTKYQSVYVSEKDECIATEV 578
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NRW PUB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Sequence 9, Appli Sequence 346, App Sequence 346, App	Sequence 346, App Sequence 346, App
US-09-995-593A US-10-1040-608 US-10-1040-609 US-10-110-049 US-10-123-904 US-10-176-918 US-10-176-918 US-10-176-918 US-10-176-918 US-10-176-918 US-10-176-918 US-10-140-474 US-10-142-419 US-10-142-419 US-10-142-419 US-10-142-419 US-10-123-262 US-10-123-262 US-10-123-263 US-10-123-264	
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ALIGNMENTS

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Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTERQ VERSION
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/908,322
FILING DATE: 17-JU1-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 7326-123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
                    Sequence 13, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
APPLICANT: 18h-Horowicz, David
US-09-908-322-13
```

Sequence 4, Appli Sequence 5, Appli Sequence 108, App Sequence 108, App Sequence 21, Appl

US-09-783-931-12 US-10-417-719-4 US-10-417-719-5 US-10-042-865-108 US-09-828-366-21

us-09-783-931-13.rapb

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481 RLKQKPECETETMNNLANCQREKDSSIGATQIKNTNKKDFHDKKVRYPVDYNLVLKVHKK 540
                                                                                         COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
FILING DATE: 15-Feb-201
CLASSIFICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INPORMATION:
NAMB: ANTIER: AGTiane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7326-122
TELEFPONEY: 212-869-8644
TELEFAN: 212-869-8644
TELEFAN: 212-869-8644
TELEFAN: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 3383; DB 1
100.0%; Pred. No. 3e-238;
tive 0; Mismatches (
  Edmonds LLP
of the Americas
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
ADDRESSEE: Pennie & STREET: 1155 Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 578; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGRLLASALLCVSGVFELKLQEFVNKKGLLNRNCCRGGGCCTFFRVCLKHYQASVSPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 GEKCPGWKGQYCTPICLPGCDQHGCDKPGECKCRVGWQGRYCDECIRYPGCQQOPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 PCNGACVDLGNSYCCQAGFGRCDNVDDCASPCNGGTCDVNDSCTCPPGYGRNCSPVSRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGRLLASALLCVSGVFELKLQEFVNKKGLLNRNCCRGGGCCTFFRVCLKHYQASVSPEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEKCPGWKGQYCTPICLPGCDQHGCDKPGECKCRVGWQGRYCDECIRYPGCVHGTCQQPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQGSYTCSCRPGYTGCEEECPCKNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPCHNGATCHRRYCECAGYGGNCQFLLPEPPGPVDEEQFPWAVCAGLVLLLGCAAVVCV
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                          Length 578;
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                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 3383; DB 9;
Best Local Similarity 100.0%; Pred. No. 3e-238;
Matches 578; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 CSEEKALRKRPSVYSTSKDTKYQSVYVSEKDECIATEV
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Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-908-322-13
     TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
                                               TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 578 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grace
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US-09-783-931-13
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                                                                                                                                                       1 MGRLLLASALLCVSGVFELKLQEFVNKKGLLNRNCCRGGGCCTFFRVCLKHYQASVSPEPP
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                                                               Gaps
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Length 578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         671 CETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
                                                191 YGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGFCDKPGEC
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                                                                                                                                              251 KCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGAT
                                                                                                                                                                                         CTNTGQGSYTCSCRPGYTG--CE----EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C
                                                                                                                                                                                                                               311 CTNTGQGSYTCSCRPGYTGSSCEIEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                     418 RCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV------DEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT
                                                                                                                                                                                                                                                                       BLSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     459 FPW-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANCQREKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grey, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND PRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09783931
; Publication No. US20030073620A1
; GENERAL INFORMATION:
; APPLICANT: 18h-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Americas
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FILING DATE: 15-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Ameri
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASEQ VERSION 2.0
CURRENT APPLICATION DATA:
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ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGOOOCDCKTFFRVCL 70
                                                                                                                                                                                                                                                                                                                                           Gray, Grace
INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 KHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWPGTFSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LASALLC-----VSGVFELKLQEFVNKKGLL-NRNCCRGG-------CCTFFRVCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 728;
                                                               578
                                                                                       CSEEKALRKRPSVYSTSKDTKYQSVYVSEKDECIATEV 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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Pred. No. 5.6e-173;
9; Mismatches 19;
                                                             CSEEKALRKRPSVYSTSKDTKYQSVYVSEKDECIATEV
                                                                                                                                                                                                                                                             APPLICANT: 18h-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-799-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-JU1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown

MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-908-322-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACIBLE
                                                                                                                                                                                                     Sequence 2, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 728 amino acids
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TELEX: 66141 PENNIE
ON FOR SEQ ID NO: 2:
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76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
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                                                                                                                                                               RESULT 3
US-09-908-322-2
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Best Local S
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671 CETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 728
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                                                                                                                                                                                                            Indels 144;
                                                                                                                                                                                     Length 728;
                                                                                                                                                                                                                                      LASALLC----VSGVFELKLQEFVNKKGLL-NRNCCRGGG
                                                                                                                                                                                  Query Match 73.6%; Score 2489; DB 10; Best Local Similarity 76.0%; Pred. No. 5.6e-173; Matches 546; Conservative 9; Mismatches 19;
REFERENCE/DOCKET NUMBER: 7326-122
                                  TELEX: 6614 PENNIE

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 728 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-783-931-2
         TELECOMMUNICATION INFORMATION
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
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Sequence 8, Application US/10417719
Publication No. US20030180784A1
GENERAL INFORMATION:

RESULT 5 US-10-417-719-8

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671 KCETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV 729
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                                                                                  THEREOF
            APPLICANT: MCGATTHY, Sean
APPLICANT: MCGATTHY, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA AND USES THE
TITE REPERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 1997-06-11
SPRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PREESEQ for Windows Version 4.0
APPLICANT: Millennium Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 75.9
Matches 546; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Gallus Gallus
US-10-417-719-8
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                                                                                                                                                         -CELSAMICADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367
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Publication No. US20040171148A1

Publication No. US20040171148A1

Publication No. US20040171148A1

Publication No. US20040171148A1

APPLICANT: Schmitt, Thomas M.

TITLE OF INVENTION: Cell Preparations Comprising Cells of the T Cell

TITLE OF INVENTION: Lineage and Methods of Making and Using Them

FILE REFERENCE: 2223-171

CURRENT APPLICATION NUMBER: US/10/731,741

CURRENT PILING DATE: 2003-12-10

PRIOR APPLICATION NUMBER: 60/432,525

PRIOR APPLICATION NUMBER: 60/432,525

PRIOR APPLICATION NUMBER: 60/432,525

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 722
                                                                                                                                                                                                                                                                                                                                                                              481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQPLLPEPPPGPMVVDLSERHMESQG
HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG
                                181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG
                                                                   ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-731-741-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.9%; Score 2466; DB 15;
llarity 76.6%; Pred. No. 2.6e-171;
Conservative 6; Mismatches 19;
                              Sequence 107, Application US/10042865 Publication No. US20040029216A1 GENERAL INFORMATION: APPLICANT: Padigaru, Muralidhara
                                                                                                                               Camman, Stacie John Shanoy, Suresh G Spytek, Kimberly Shong, Mei Gangolli, Esha A Burgess, Catherine E Patturdam, Meera Vernet, Corine A.M Tcherney, Velizar T Miller, Charles E Guo, Xiaojia E Guo, Xiaojia E Boldog, Ference L Grosse, William M Alsobrook II, John P Gerlach, Valerie L Edinger, Shlomit R Rothenberg, Mark E Ellerman, Karen MacDougall, John Malyankar, Uriel M Smithson, Glennda Shinker, Erik
                                                                                                    Li, Li
Zerhusen, Bryan D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus
US-10-042-865-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 553; Conserval
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APPLICANT:
APPLICANT:
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72.8%; Score 2462; DB 9;
llarity 75.9%; Pred. No. 5.2e-171;
Conservative 6; Mismatches 24;
           APPLICATION DAMER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION AURIER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY, AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE DOCKET NUMBER: 18,872
REFERENCE DOCKET NUMBER: 7326-123
TELECHONE 212-790-9090
TELECHONE: 212-790-9090
TELEPKX: 212-869-8864
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  NO: 12
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                       LENGTH: 722 amino acids
                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 548; Conserv
   CURRENT
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LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE
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INVENTION: NUCLECTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED
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Henrique, Domingos Manuel Pii
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde LLP
STREET: 1155 Avenue of the Americ TIY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: PASTSEQ VERSION 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/09908322
Patent No. US20020107194A1
GENERAL INFORMATION:
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US-09-908-322-12
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121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE 180
                                                                                                                                241 ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
                                                                                                                                                                                      -CELSAMICADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367
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                                                    181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGOYCTDPICLPGCDDOHGYCDKPG
                                                                                                 210 ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG
                                                                                                                                                                   ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFYGK
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Pred. No. 2e-170;
6; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 72.5%;
Best Local Similarity 76.4%;
Matches 551; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mus Musculus
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EV 722
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                   661 RDTKCQSQSLQEKRRSPQHLGVGRFLTENRPESVYSTSKDTKYQSVYVLSAEKDECVIAT 720
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                                                                                                                                                                             Sequence 12, Application US/09781931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: ISH-Horowicz, David
APPLICANT: ISH-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
AND FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels 144;
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Pred. No. 5.2e-171;
6; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/783,931
FILING DATE: 15-Feb-2001
CLASSIFICATION AUMBER: 08/981,392
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: ANTIEL AGTISHE M.
REGISTRATION NUMBER: 32,605
TELEPRIONE: 212-790-9090
TELEPRIOR: 212-869-8864
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: <Unknown>
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INFORMATION FOR SEQ 1D NO: 12:
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Best Local Similarity 75.9
Matches 548; Conservative
537 VHKKCSEEKALRKR
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EV 722
                                                                EV 578
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US-09-783-931-12
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Gaps

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TCTNTGGGSYTCSCRPGYTGANCELEVDECAPSPCKNGGSCTDLEDSYSCTCPPGFYGKV 360
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                                                                                                                                                                                                                                         61 VCLKHYQASVSPEPPCTYGSAVTAVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS
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                                                                                                                                                                    VCLKHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG-DPAFSNPIRFPFGFTWPGTFS
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                                                                                         Length 713;
                                                                                                                        135;
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                                                                                         72.3%; Score 2447.5; DB 14; Lengt
75.7%; Pred. No. 5.8e-170;
ive 9; Mismatches 29; Indels
                                                                                                                                                     1 MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG
            LENGTH: 713
TYPE: PT
ORGANISM: Rattus No. US20030180784Alvegicus
US-10-417-719-5
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Publication No. US20040029216A1
GENERAL INFORMATION:
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Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
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Zerhusen, Bryan D
                                                                                                         Local Similarity 75.7
nes 540; Conservative
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US-10-042-865-108
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                                                                                            Query Match
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                             9
                 1 MGRRSALALAVVSALLCQVWSSGVFELKLQEFVNKKGLLGNRNCCRGGSGPPCACRTFFR
                                                                                                                                                                                                                                                                  -FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PB-C--ETETMNNLANCQREKD
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                                                                                                                        LIIEALHTDSPDDL-TENPERLISRL-TQRHLVGEEWSQDLHSSGRTDL-YSYRFVCDEH
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MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG
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APPLICANT: McCarthy, Sean
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TILE ON TOWERTION: HUMAN DELTA3 AND USES THE
FILE REFERENCE: MBIO1997-002CP2M
CURRENT APPLICATION NUMBER: US/09/417,719
CURRENT APPLICATION NUMBER: US/09/568,218
PRIOR APPLICATION NUMBER: US/09/68,218
PRIOR PILING DATE: 1997-06-11
PRIOR PILING DATE: 1997-06-11
PRIOR PILING DATE: 1997-06-11
PRIOR PILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/10417119
Publication No. US20030180784A1
GENERAL INFORMATION:
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US-10-417-719-5
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361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCSSSPCSNGAKCV 420
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APPLICANT: Genemetech, Inc.
APPLICANT: Goodeard, Addrey
APPLICANT: Goodeard, Addrey
APPLICANT: Goodeard, Addrey
APPLICANT: Naples: Mary
APPLICANT: Naples: Mary
APPLICANT: Naples: Mary
APPLICANT: Wood, William I.
APPLICANT: Woo
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                                                                                                                                                                                                                                                                                                                                                                           CAGLV---LLLLGCAA-VVCVRLK----QKP--EC--ETETMNNLANCQREKD---SSIG
                                                                                                                                                                                                                        416 VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPPGPV----DEEQFPW-AV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09828366
Patent No. US20020010137A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-828-366-21
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LENGTH: 723
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APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Smithson, Glennda
APPLICANT: Scone, David
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT APPLICATION NUMBER: US/266,417
PRIOR APPLICATION NUMBER: 60/266,417
PRIOR APPLICATION NUMBER: 60/266,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
PRIOR PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
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                                                                                                                                                                      Guo, Xiaojia
Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
                                                                                                        Tchernev, Velizar T
Miller, Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Rattus norvegicus US-10-042-865-108
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                                                                                                               253 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCKNGATCTNTGQGSY
                                                                                                                                                                                              TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD
                                                                                                                                                                                                                          313 TCSCRPGYTGATCELGIDECDPSPCKNGGSCTDLENSYSCTCPPGFYGKICELSAMTCAD
                                                                                                                                                                                                                                                                                                     GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CO
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CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR APPLICATION NUMBER: 60/059117
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Publication No. US20030004311A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Beres, Kevin P.
APPLICANT: Beres, Kevin P.
APPLICANT: Beres, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gadard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grareon
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Wictoria
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
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                                                                                                                                           GPCFNGGRCSDSPDGGYSCRCPVGYSGFNCEKKIDYCSSSPCSNGAKCVDLGDAYLCRCQ 432
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        TCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
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APPLICANT: TOCH, AKIRA
ITILE OF INVENTION: DIFFRENTIATION-SUPPRESSIVE POLYPEPTIDE
FILE REFERENCE: KP6447DIV
CURRENT APPLICATION NUMBER: US/09/995,593A
CURRENT PILING DATE: 2002-02-28
FRIOR APPLICATION NUMBER: US/086,740
FRIOR FILING DATE: 1998-06-18
FRIOR PELLING DATE: 1998-06-18
FRIOR APPLICATION NUMBER: UP 7-29611
FRIOR APPLICATION NUMBER: UP 7-311811
FRIOR APPLICATION NUMBER: UP 7-311811
FRIOR APPLICATION NUMBER: DF 7-311811
FRIOR FILING DATE: 1996-11-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09995593A Patent No. US20020128197A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-995-593A-9
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US-09-995-593A-9
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1997-09-17 NUMBER: 60/059184 1997-09-17 NUMBER: 60/059263 1997-09-18 NUMBER: 60/059352 1997-09-19 NUMBER: 60/05988 1997-09-19 NUMBER: 60/05936 1997-09-24 NUMBER: 60/05936		98-02-04
FILING DATE: APPLICATION PELING DATE: APPLICATION PELING DATE: APPLICATION PELING DATE: APPLICATION PELING DATE: APPLICATION	PALLING DATE APPLICATION FILLING DATE FILLING DATE APPLICATION FILLING DATE FILLING DATE APPLICATION FILLING DATE FILLING	ILING DATE:
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PRIOR APPLICATION NUMBER: 60/074092
PRIOR PAPLICATION NUMBER: 60/07491
PRIOR PALLING DATE: 1998-02-09
PRIOR PALLING DATE: 1998-03-12
PRIOR PAPLICATION NUMBER: 60/079910
PRIOR PAPLICATION NUMBER: 60/079910
PRIOR PAPLICATION NUMBER: 60/07924
PRIOR PAPLICATION NUMBER: 60/07924
PRIOR PAPLICATION NUMBER: 60/07924
PRIOR PAPLICATION NUMBER: 60/09129
PRIOR PAPLICATION NUMBER: 60/09139
PRIOR PAPLICATION NUMBER: 60/09130
PRIOR PAPLICATION NUM

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GPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDLGNSY-C-CQ 376
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR APPLICATION NUMBER: 60/08947
PRIOR APPLICATION NUMBER: 60/090349
PRIOR PELING DATE: 1998-06-23
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
PRIOR PELING DATE: 1998-07-02
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Best Local Similarity 75.1%
Matches 534; Conservative
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KNTNKK-DFH----DK---KVRYP-VDYNLV-------LKVHKKC----S

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492

372

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Gaps

26 72

Search completed: November 29, 2004, 13:42:04 Job time : 62.226 secs

us-09-783-931-13.rpr

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5.1.6
Compugen Ltd.
version 5
GenCore (c) 1993
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Bw model - protein search, using OM protein

November 29, 2004, 13:16:29 ; Search time 14.4855 Seconds (without alignments) 3839.238 Million cell updates/sec Run on:

US-09-783-931-13 3383 1 MGRLLASALLCVSGVFELKL......DTKYQSVYVSEKDECIATEV 578

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 88 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ptj	C-Delta-1 - chicke	DELTA-like 1 - mou	Delta-4 protein -	Delta-4 protein -	gene Delta protein		neurogenic repetit	jagged protein pre	gene serrate prote	transmembrane prot	Xotch protein - Af	homeotic protein d	notch-1 protein -	Motch B protein -	notch protein homo	preadipocyte facto	cell-fate determin	notch homolog - se	notch 3 protein -	delta-like homeoti	notch protein homo	Notch homolog prot	fibropellin Ia - s	epidermal growth f	notch protein - fr	notch3 protein - h	. crumbs protein - f	notch4 - mouse	Notch homolog Moto
SUMMARIES		150719	148324	JC7570	JC7569	S19087	A31246	800670	A56136	S16148	S42612	A35844	S53718	A46019	A49175	S18188	A54785	A49128	T31070	S45306	S53716	A40043	T30201	A40136	JC7125	A24420	S78549	A35672	905	A48825
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	Query Match Length	728	722	685	686	833	832	880	1220	1408	2437	2524	385	2531	1203	2531	385	2471	2531	2318	383	2555	2352	1064	308	2703	2321	2139	1964	861
de	Query Match		2	39.3	38.4	'n	32.1	32.1	27.7	22.4	14.7	4.	14.5	•	4	•	14.3	14.1	14.0	13.7	•	13.6	٠	•		٠	•	13.0	٠	12.5
	Score	2489	2466	1329.5	1298.5		1085.5	1084.5	935.5	758.5	496.5	492.5	a.	489.5	485	484.5	484	478	473.5	464	461	459	456.5	454	450	T#	445.5		434	424.5
	Result No.	П	7	m	4	S	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	29

glpl protein precu	homeotic protein 1	hypothetical prote	protein F11C7.4 [i	MEGF6 protein - ra	adhesive plaque pr	tenascin-C - human	fibropellin C prec	tenascin precursor	hypothetical prote	tenascin precursor	tenascin-X precurs	probable tenascin	hypothetical prote	tenascin precursor	tenascin-x - bovin
A32901	S06434	T27283	E89753	T13954	A56175	A32160	A48836	JQ1322	T25933	819694	A40701	T09070	T26972	A32230	T42629
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ALIGNMENTS

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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 11-Sep.1996 #sequence_revision 13-Sep.1996 #text_change 09-Jul-2004
C;Date: 10-Sep.1996 #sequence_revision 13-Sep.1996 #text_change 09-Jul-2004
C;Date: 10-Sep.1996 #sequence_revision: 150719
R;Henrique, D: Adam, J: Myat, A.; Chitnis, A.; Lewis, J.; Ish-Horowicz, D.
A;Title: Expression of a Delta homologue in prospective neurons in the chick.
A;Reference number: 150719; MUID:95319507; PMID:7596411
A;Reference number: 150719; MUID:95319507; PMID:7596411
A;Reference number: Iso719
A;Reference number: Espression: Es
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LASALLC-----VSGVFELKLQEFVNKKGLL-NRNCCRGGG------CCTFFRVCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19; Indels 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.6%; Score 2489; DB 2; Length 728; 76.0%; Pred. No. 1.1e-145; ive 9; Mismatches 19; Indels 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.0°
Matches 546; Conservative
                                                                     C-Delta-1 - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159
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RESULT 1
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CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318 CTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNC 370

251 271 311 319

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ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369

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Delta-4 protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JC7570
R;Yoneya, T.; Tahara, T.; Nagao, K.; Yamada, Y.; Yamamoto, T.; Osawa, M.; Miyatani, S.; P. J. Blochen. 129, 27-34, 2001
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Title: Molecular cloning of Delta-4, a new mouse and human notch ligand.
A;Reference number: JC7569; MUID: 21064937; PMID:11134954
A;Recession: JC7570
A;Molecule type: mRNA
A;Residues: 1-685 < YON>
A;Cross-references: UNIPROT:O9NR61; DDBJ;AB043894
C;Cross-references: UNIPROT:O9NR61; DDBJ;AB043894
C;Coment: This protein, the growth or differentiation of vascular endothelial cells.
C;Genetics:
C;Genetic
                                                                                                                                                                                                                                            540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
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                                                                                                                                          DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGICRDSVNDFSCTCPPGYTGKNCSAP
                                                                                                                                                                                                                                                                                                                                                                                              D---SSIGATQIKNTNKK-DFHDK------KVRYP-VDYNLV--LK------VHKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 SGVFQLQLQEPINERGVLASGRPC--EPGCRTFFRVCLKHFQAVVSP-GPCTFGTVSTPV
-CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV
                              361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GRGEKCPGWKGQYC-TPICLPGC-DQHG-CDKPGECKCRVGWQGRYCDECIRYPGCVHG
                                                                                                                                                                                                                                                                                            --FPW-AVCAGLV---LILLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----CSEEKAL-----RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT
                                                                                                                                                                                             VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----BEQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGVFELKLQEFVNKKGLL - - NRNCCRGGGCCTFFRVCLKHYQASVSPEPPCTYGS - ATPV
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                                                                                              DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
39.3%; Score 1329.5; DB 2; Length
Best Local Similarity 46.4%; Pred. No. 1.6e-74;
Matches 314; Conservative 81; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EV 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRESULT 2
148124
DELTA-like 1 - mouse
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #text_change 09-Jul-2004
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C.Accession: 148324
R.Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A.
Development 121, 2407-2418, 1995
A;Title: Transient and restricted expression during mouse embryogenesis of Dll1, a murin
A;Reference number: 148324; MUID:95401858; PMID:7671806
A;Accession: 148324
A;Estus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-722 <RES>
A;Residues: 1-722 <RES>
A;Cross-references: UNIPROT:Q61483; EMBL:X80903; NID:g8065569; PIDN:CAA56865.1; PID:g8065
                                                                                                                                                                                                                                                                                               610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SSIGATQIKNTNKK-DFH----DK---KVRYP-VDYNLVLKV------HKKC--- 541
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  ELSAMTCADGPCFNGGRCTDNPDGGYSCRCPLGYSGFNCEKKIDYCSSSPCANGAQCVDL
                                                                               RCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV------DEEQ
                                                                                                                                                                                                                                                 FPW-AVCAGLVL---LLLGCAA-VVCVRLK----QKPEC---ETETMNNLANCQREKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CETYDSEAEEKSAVQLKSSDTSERKRPDSVYSTSKDTKYQSVYVISEEKDECIIATEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SEEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: Dlll
;Superfamily: delta-4 protein; EGF homology
;331-362/Domain: EGF homology <EGF2>
;446-477/Domain: EGF homology <EGF>
;488-515/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                               551
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Qy 321 HCELGLSKCASNPCRNGGSCKDQENSYHCLCPPGFYGCHCCELSAMTCADGPCFNGGSCRC336 Db 321 HCELGLSKCASNPCRNGGSCKDQENSYHCLCPPGYYGQHCEHSTLTCADSPCFNGGSCRE 380 Qy 337 DNPDGGYCCPLGSGRNCEKK-DC-SSPCNGACVDLGNSYCCQAGFGRCD-383 Db 384 NVDDCA-SPC-NGGTCEKKVDRCTSNPCANGGCQNRGPSRTCRCRPGFTGTHCEL 440 Qy 384 NVDDCA-SPC-NGGTC-DVNDSCTCPPGY-GRNCSPVSRCEHPCHNGATCH-430 1:	RESULT 5 919087 Gene Dalta protein precursor - fruit fly (Drosophila melanogaster) C,Date: 20-62-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 C,Date: 20-62-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 C,Accession: 519087 R,Muskardtoh, MA. R,Maskardtoh, MA. R,Accession: 519087 A,Reference number: 519087 A,Ref
QY 292	RESULT 4 JCTS69 Delta-4 procein - mouse CiSpeciae: Mus maculua (house mouse) CiSpeciae: Mus maculua (house) CiSpeciae: Mus maculua (house) A; Notaca: T: Mosgao, K:; Yamada, Y:; Yamamoto, T:; Osawa, M.; Miyatani, S:; M; Parker and Mus and M

593

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ATCINIGOGSYTCSCRPGYTG--CEEE------CPCKN 298
                                                                                                                                     305 GTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCRN 364
                                                                                                                                                                                                                                                                                                             --GRCDN-VDDC-ASPC-NGGIC-DVND--SCTCPPGY-GKNCS-PVSRCEH-PCHNGAT 428
                                                                                                                                                                                                                                                                                                                               484 HGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHNGGT 543
                                                                                                                                                                                                                                                                                                                                                                             365 GWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSP 424
                                                                                                                                                                                                                                                                            425 NPCINGGSC-QPSGKCICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCVPGF 483
                                                                 ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG
                                                                                                                                                                                                                                                                                                                                                                                                             544 CMNRVNSFECVCANGFRGK-------QCDEESYDSVTFDAHQYGATTQARADGLANA
                                                                                                                                                                                                                                                                                                                                                                                                                                             -----WAVCAGLVLLLLGCAAVVCVRLKQKPECETETMINLANCQREKDSSIGATQIK
                                                                                                                                                                                                                                              GPCFNGGRCDNPDGGYCCPLG-SGFNCEKK--DC-SSPC--NGACVDLGNSYCCQA--GF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.1;
Best Local Similarity 37.9;
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
A31246
metagenic protein Delta precursor - fruit fly (Drosophila melanogaster)
c)species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C;Accession: A31246
C;Accession: A31246
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes A;Accession: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Residues: 1-832 <KOP>
C;Genetics:
A;Gene: FlyBase:Dl
                    305 GTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCHCAN 364
                                                                                                                                                    365 GWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSP 424
                                                                                                                                                                                                379
                                                                                                                                                                                                                               483
                                                                                                                                                                                                                                                             380 --GRCDN-VDDC-ASPC-NGGTC-DVND--SCTCPPGY-GKNCS-PVSRCEH-PCHNGAT 428
                                                                                                                                                                                                                                                                                460
                                                                                                                                                                                                                                                                                                                                                  -----WAVCAGLVLLLGCAAVVCVRLKQKPECETETMNNLANCQREKDSSIGATQIK 513
                                                                                                                                                                                                                                                                                                                                                                                                                65 FRLCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSFSWPG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 TFSLIIEALHTDSPDDLTENPERLISRLTQRHL--VGEEWSQDLHSSGRTDL-YSYRFVC 154
                                                                                                                                  -----SCTD----SCTD-----LES----SCTCPPGFYG-KCELSAMTCAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 TFSLIVEAMHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 DEHYYGEGCSVFCRPRDD-FGHFTCGR-GE--KCPGWKGQYC-TP1CLPGCDQHGCDKPG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
   ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG
                                                                                                                                                                                                GPCFNGGRCDNPDGGYCCPLG-SGFNCEKK--DC-SSPC--NGACVDLGNSYCCQA--GF
                                                                                                                                                                                                                   425 NPCINGGSC-QPSGKCICPAGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCVPGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRVCLKHYQASVSPEPPCTYGSA-TPVLGSFSPDGAG----DPAFSNPIRFPFGFTWPG
                                                                                                                                                                                                                                                                                                                               CHRRY----CECA-GYGGNCQFLLPEPPGPVDEEQFP---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 RLLASALLCV-----SGVFELKLQEFVNKKGLLNR-NCCRG------GGCCTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1085.5; DB 2; Length 832;
; Pred. No. 1.8e-59;
68; Mismatches 178; Indels 165;
                                                                   269 ATCTNTGQGSYTCSCRPGYTG--CEEE---C---PCKNG----
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C;Superfamily: neurogenic protein delta;
F;295-328/Domain: EGF homology «EGXI»
F;422-450/Domain: EGF homology «EGFI»
F;457-488/Domain: EGF homology «EGF»
F;533-564/Domain: EGF homology «EGF»
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Best Local Similarity 37.8%;
Matches 250; Conservative 6
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S00670

Bourcogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)

NyAlternate names: gene Dl protein
CiSpeciae: Drosophila melanogaster
CiDate: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
CiAccession: S00670; A26637
CiAccession: S00670; A26637

RyVaessin, H.; Bremer, K.A.; Knust, B.; Campos-Ortega, J.A.
EMBO J. 6, 3431-3440, 1897
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic
A;Reference number: S00670
A;Accession: A266, 1987
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and that ceremic number: A1081; MUD:87218537; PMD:3107986
A;Accession: A26637
A;Accession: A2640
A;Cross-references: GB:X05140; NID:G7851; PIDN:CAA28786.1; PID:g929563
C;Gopertani: Delta; Dl
A;Cross-references: FlyBase:FBgn0000463
C;Gopertani: Delta; Dl
A;Cross-references: FlyBase:FBgn0000463
C;Gopertani: Bignal sequence #status predicted <SIG>
C;Gopertani: EGF homology <EGF>>
F;19-18/Domain: EGF homology <EGF>>
F;457-488/Domain: EGF homology <EGF>>
F;533-564/Domain: EGF homology <EGF>>
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F;85-1221/Domain: extracellular #status pred	44 FRVCLKHYQASVSPEPPCTYGS-ATPVLGSFSPDGAGDPAFSNPIRFPFGFTWPGT 98
C;Keywords: glycoprotein; transmembrane prote F;1-84/Domain: signal sequence #starus predit F:85-1408/Product: gene serrate protein #stan	
C;Genetics: A;Gene: FlyBase:Ser A:Genera-raferences: FlyBase:FRon0004197	SLASALLCVSGVFEL
A; Residues: 1-15,20-26,'A',28-1408 <fle> A; Cross references: GB:M35759; NID:g158605;</fle>	5
A;Accession: A35555 A;Status: preliminary A;Molecule tvoe: mRNA	r;494-52J.Domain: EGF homology <egf>> F;634-665/Domain: EGF homology <egf2></egf2></egf>
A,Title: The gene Serrate encodes a putative A,Reference number: A36666; MUID:91099666; Pl	Cross-references: GB:LJ38483 379-41/Jonain: EGF homology <egfl></egfl>
R, Fleming, R.J.; Scottgale, T.N.; Diederich, Genes Dev. 4, 2188-2201, 1990	Molecule type: mRNA Residues: 1-1220 <lin></lin>
A; Residues: 1-1351, 'T', 1353-1408 <tho2> A; Gross-references: EMBL; X56811; NID: 98563;</tho2>	Accesion: A56136 Status: preliminary
A;Accession: S16878 A;Molecule type: mRNA	Title: Jagged: a mammalian ligand that activates Notchl. Reference number: A56136; MUID:95211842; PMID:7697721
submitted to the EMBL Data Library, November A; Reference number: \$16878	Lindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G. 11 80, 909-917, 1995
A; Cross-references: UNIPROT: P18168; EMBL: X56 R: Thomas. U.	opter. 29. Apr.1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003 Accession: A55136
A; Molecule type mRNA	9ged protein precursor - rat
A,Title: The Drosophila gene Serrate encodes A;Reference number: S16148; MUID:91347903; P	TINS .
R; Thomas, U.; Speicher, S.A.; Knust, E. Development 111, 749-761, 1991	596 VLIAVFSVAMPLVAVIAAC-VVFCMKRKRRAQEKDNAEARKQNEQNAVATMHHN 649
C. Date: J. D. Decopilla metamogaster C. Date: J. Decopy Headuence revision 02-Au	461WAVCAGLVLLLGCAAVVCVRLKQKPECETETWANLANCQREKDSSIGATQIKN 514
gene errate protein precursor - fruit fly (Db 546 NRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQV 595
RESULT 9	431 RRYCECA-GYGGNCQFLLPEPPGPVDEEQFP
Db 550 CKCPEDYEGKNCSHL 564	THCSSKVDLCLIRPCANGGTCLNLANDYQCTCRAGFTGKDCSVDIDBCSSGPCHNGGTCM
Qy 434 CECAGYGGNCOFL 446	Db 427 CINGGSC-QPSGKCICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCVPGFHG 485
490	330 CFNGGRCDNPDGGYCCPLG-SGFNCEKKDC-SSPCNGACVDLGNSYCCQAGF
DD 430 NELASIXCUCLERGRANGUNCUININUCLEGGG	Db 367 SGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNCSPNP 426
338	300SCTDLEŞSCTCPPGFYG-KCELSAMTCADGP 329
Db 370 PTCSTNIDDCSPNNCSHGGTCQDLVNGFKC	CENTGEGLYTCKCAPGYSGDDCENELYSCDADVNPCONGGTCIDEPHTKTGXKCHCRNGW
Qy 298Qy 298	271 CTNTGOGSYTCSCRPGYTGCREE
310	Qy 212 KCRVGWGGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT 270
2 2 2	Db 187 NYYGSGCAKFCRPRDDSFGHSTCSETGEIICLIGWQGDYCHIPKCAKGCEHGHCDKFNQC 246
. Qy 209 GECKCRVGWQGRXCDECIRYPGCVHGTCQQ	VECRPRDD-
190	Db 127 SLIVEAWHDTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDFRVTCDL 186
156	
Qy 99 FSLIIEALHTDSPDDLTENPERLISKLTQR 133 YHLINDS - MOCCOND-TIODECTTERS OF	Qy 46 VCLKHYQASVSPEPPCTYGSA-TPVLGSFSPDGAGDPAFSNPIRFPFGFTWPGTF 99
Db 76 FKVCLKEYQSRVIAGGPCSFGSGSTPVIGG	r vo
	5 LASALLCVGGUFELKLOEFVNKKGLIANE-NCCRGGGCCTFFF 45

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ss an BGF-like transmembrane protein with a со:
PMID:1840519
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PMID:2125287
                                                          GGNTFNLKASRGND----RNRIVLPFSFAWPRS 132
                                         DRHLV--GEEWSQDLHSSGRTDL-YSYRFVCD 155
                                                                                            KK--CPGWKGQYCT-PICLPGCD-QHG-CDKP 208
                                                                                                             ODPWOCNCOEGWGGLFCNODLNYCTHHKPC-N 267
                                                                                                                                                                                                         ----- CEB---- 297
                                                                                                                                                                                                                        |:| | | HACLSDPCHNRGSCKETSSGFECECSPGWTG 369
                                                                                                                                                                                                                                                           SCTCPPGFYGK-CELSAMTCADGPCFNGGRCD 337
                                                                                                                                                                                                                                                                                                               C--NGACVDLGNSY--CCQAGFG--RCD-NV 385
                                                                                                                                                                                                                                                                                                                                   GKN-CS-PVSRCE-HPCHNGATCHRR----Y 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ug-1994 #text_change 09-Jul-2004
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1, R.J.; Artavanis-Tsakonas, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Drosophila melanogaster)
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sdicted <SIG>
status predicted <MAT>
edicted <EXT>
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transmembrane protein precursor - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Species: Brachydanio rerio (zebra fish)
C;Accession: $42612
R;Bierkamp, C:;Campos-Ortega, J.A.
Mach. Dev. 43, 87-100, 1993
A;Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern of A;Reference number: $42612; MUID:94128602; PMID:8297791
A;Accession: $42612; MUID:94128602; PMID:8297791
A;Reference number: $42612; MUID:94128602; PMID:8297791
A;Status: preliminary
A;Residues: 1-2437 < ABIE>
A;Status: preliminary
A;Residues: 1-2437 < ABIE>
A;Coss-references: UNIPROT:P46530; EMBL:X69088; NID:9433866; PIDN:CAA48831.1; PID:943386
A;Coss-references: UNIPROT:P46530; EMBL:X69088; NID:9433866; PIDN:CAA48831.1; PID:943386
B;1053-1054/Domain: EGF homology < EGF>
F;1015-1947/Domain: ankyrin repeat homology < ANI>
F;1915-1947/Domain: ankyrin repeat homology < ANI>
F;1915-2014/Domain: ankyrin repeat homology < ANI>
F;2018-2014/Domain: ankyrin repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GFHCVCVNGWTGDDCS---ENIDDCASAACSHGATCHDRVASFPCECPHGRTGLLCHLDD 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434 SFQCKCLQGYEGPRCEMDVNECKSNPCQNDATCLDQIGGFHCICMPGYEGVFCQINSDDC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 ASQPCLNGKCIDKINSFHCECPKGFSGSLCQVDVDECA-STPCKNGAKCTD-GPNKYTCE 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPCANGGOCSAFE---SHYICTCPPNFHGQTCRQDVNECAVSPSPCRNGGTCINEVGSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 VDDCTQHACENGGPCIDGINTYNCHCDKHWTGQYCTEDVDECELSPNACQNGGTCHNTIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRPGYTG--CE---BEC---PCKNGSCTDLESS--CTCPPGFYGK-CELSAMTCADGPCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YCEC-AGYGG-NCQFLLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ECKCRVGWQGRYCD--------ECIRYPG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indele
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.7%; Score 496.5; 25.3%; Pred. No. 6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCCRGGGCCTFFRVCLKHY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.33
Matches 180; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEGCSVFCRPRDD-FGHFTCG-RGEK--CPGWKGQYC-TPICLPGCDQ-HG-CDKPGECK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 NTTCTTFCRPRDDQFGHYACGSEGQKLCLNGWQGVNCERAICKAGCDPVHGKCDRPGECE 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- CTCPPGFY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 ISAAGNFELEILEISNTNSHLLNGYCCGMPAELRATKTIGCSPCTTAFRLCLKEYQTTEQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ASVSPEPPCTYGSA-TPVLGS----FSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIEAL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425 RSNMGRPVRRSSSMRSLDHLRPEGQALNGSSSSGLVSLGSLQLQQQLAPDFTCDCAAGWT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||:|| :|| :|| :|| CASIS--TGCSFGNATTKILGGSSFVLSDPGVG-----AIVLPPTFRWTKSFTLILQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| || :| || || || DMYNTSYPD----AERLIEETSYSGVILPSPEW-KTLDHIGRNARITYRVRVQCAVTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||:: || ||| :|| || 485 GPTCEINIDECAGGPCEHGGTCIDLIGGFRCECPPEWHGDVCQVDVNECEAPHSAGIAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LCVSGVFELKLQEFVNKKG-LLNRNCC------RGGGCCTFFRVCLKHYQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRVGWQGRYCDECIRYPGCVHGTCQ-QPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        545 ALLTTTATAIIGSNLSSTALLAALTSAVASTSLAIGPCINAKECRNQPGSFACICKEGWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTNTGQGSYTCSCRPGYTGCEEEC-----PCKNGSCTDLESS------
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                                                                                                                                                                                                                                                                                                                                                                                                            F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.4%; Score 758.5; DB 2; Length 1408; Best Local Similarity 31.5%; Pred. No. 3.4e-39; Matches 211; Conservative 63; Mismatches 150; Indels 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 G-KCELSAMTCADGPCFNGGRCDNPDGGY-C-CP-----
.in: EGF in.
Jain: EGF homology *.
Jomain: EGF homology *.
Jomain: EGF homology *EG05>
J8/Domain: EGF homology *EG05>
J8/Domain: EGF homology *EG05>
J8/Domain: EGF homology *EG07>
-683/Domain: EGF homology *EG07>
-720/Domain: EGF homology *EG08>
J27-796/Domain: EGF homology *EG18>
F;841-876/Domain: EGF homology *EG19>
F;841-876/Domain: EGF homology *EG11>
F;841-876/Domain: EGF homology *EG13>
F;921-052/Domain: EGF homology *EG13>
F;921-060/Region: cysteine-rich
J31,412,452,558,739,965,977,1004,17
-7,331,412,452,558,739,965,977,1004,17
-7NNCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : | LRPLCSQPP 731
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                                                                                                                                                                                                                                                      F;727-796/Domain: E;803-834/Domain: E;803-834/Domain: E;841-876/Domain: E;883-914/Domain: E;921-952/Domain: E
                                                                                                                                                   F;533-608/Domain: F;615-645/Domain: F;652-683/Domain: F;690-720/Domain: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S53718
R;Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
Biochim. Biophys. Acta 1261, 223-232, 1995
A;Title: dlk, pd2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like sup A;Reference number: S53716, MUID:95226449; PMID:7711066
A;Accession: S53718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q09163; EMBL:U15980; NID:g562107; PIDN:AAB60495.1; PID:g5621.
C;Superfamily: preadipocyte factor 1; EGF homology
C;Keywords: transmembrane protein
F;54-85/Domain: EGF homology <EGF1>
F;92-124/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 notch-1 protein - mouse
N;Alternate names: motch protein
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence revision 18-Nov-1994 #text change 16-Aug-2004
C;Accession: A46019; S25144; C49175; B46438; P46438; PHI569; S32109
R;del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid Genomics 15, 259-264, 1993
A;Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGGRCDNPDGGYCCPLGSGFNCEKKDCSSPCNGACVDLGNSYCCQAGFGRCDNVDDCAS-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PC-NGGTC----DVNDSCTC-PPGYGKNC----SPVSRCEHPCHNGATCHRRYCECAG 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | : | : | 264 YGLTYRL----TPGVHELPVQQPEQHILKVSMKELNKSTPLLTEGQAICFTILGVLTSLV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CBEBC------PCKN-GSCTDLE----SSCTCPPGFYGK-CELSAMT--CADGPCF 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 DCQHKAGPCVINGSPCQHGGACVDDEGQASHASCLCPPGFSGNFCEIVAATNSCTPNPCE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NDGVCTDIGGDFRCRCPAGF--VDKTCSRP-------VSNCASG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCQNGGTCLQHTQVSFECLCKPPFMGPTCAKKRGASPVQVTHLP-----SG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGHFTCGRGEKCPGWKGQYCTPICLPGCD-QHG-CDKPGECKCRVGWQGRYCDECIRYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCNGATCTNTGQGSYTCSCRPGYTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.5%; Score 491; DB 2; Length 385; Similarity 32.8%; Pred. No. 3.2e-23; 6; Conservative 39; Mismatches 95; Indels 1:
                                                                     CECPPGWQGQTCEIDMNECVNRPCRN-----GAT-CQNTN 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:131-167/Domain: EGF homology <EGF3>
F:214-246/Domain: EGF homology <EGX1>
F:303-332/Domain: transmembrane #status predicted <TM1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLGCAAVYCVRLKQKPECETETMN 494
                                                                                                                                                                                                                          homeotic protein dlk - mouse
    ||| || :||
810 VAGYKCNC--MLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-385 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391
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                                                                     493
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                                                                                                    A35844

Xotch protein - African clawed frog

C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Zenopus laevis (African clawed frog)
C;Species: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
C;Accession: A35844

R;Coffman, C.; Harris, W.; Kintner, C.
Science 249; 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844 MuID:90385285; PMID:2402639
A;Accession: A35844
A;Reference number: A35844 MuID:90385285; PMID:2402639
A;Accession: Botaliniarry; nucleic acid sequence not shown; not compared with conceptual trafinecial type: mRNA
A;Residues: 1-2524 cCOF>
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C;Superfamily: Notch protein;
F;146-1215/Domain: EGF homology cEGF>
F;222-224/Domain: EGF homology cEGF>
F;357-1890;Domain: EGF homology cEGF>
F;1957-1890;Domain: EGF homology cEGF>
F;1957-1890;Domain: ankyrin repeat homology cAN3>
F;1957-1890;Domain: ankyrin repeat homology cAN3>
F;1951-2023/Domain: ankyrin repeat homology cAN3>
F;2021-2023/Domain: ankyrin repeat homology cAN3>
F;2057-2089/Domain: ankyrin repeat homology cAN3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCTYGS---ATPVLGS---FSPDGAGDPAFSNPIRFPFGFTWPGTFSLIIEALHTDSPDD 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-----RDDFGHFTCGRGEKC-PGWKGQYC-TPI------CLPGCDQHGCD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ECKCRVGWQGRYCD----ECIRYPG 230
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--CASNPCL---NQGSCIDDVAGFKCNC
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N'Alternate names: Notch homolog
C;Species: Mus musculus (house mouse)
C;Dacession: A49175; PH1570; S32113
R;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of A;Reference number: A49175; MUID:93178563; PMID:8440332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    949 CASNPCQNGANCTDCVDSYTCTCPVGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTCL 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                712 TCLSEVNECNSNPCIHGACRDGLNGYKCDCAPGWSGTNC-DINNNBCESNPCVNGGTCKD 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               831 APCATSPCKNSGVCKESEDYESFSCVCPTGWOGOTCEVDINECV-KSPCRHGASCONT-N 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCHNGATCHRR----YCEC-AGYGG-NCQFLLPEPPGPVDEEQFPWAVCA---GLVLLLL 472
                                                                                                                  54
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                                                                                                                                                             CMDKIHEFQCQ----CPKGFNGHLCQYDVDECASTPCKNGAKCLDGPNTYTCVCTEGYTGT
                                                                                                                                                                                                          -----VSPEPPCTYGSATPVLGSFS----PDGAG-----DPAFSNPIRFPFGFTW
                                                                                                                                                                                                                                                                                                   PGTFS-----LIIEALHTDSP-----DDLTENPERLISRLTQRHLVGEEWSQDLHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -------RGEKC---PGWKGQYCTPICLPGCDQHGCDKPGECK-
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                                                                     Indels 247; Gaps
                       Length 2531;
                                                                                                                                                                                                                                                                                                                                              615 GGTCODRDNSYLCLCLKGTTGPNCEINLDDCASNP-----
                     14.5%; Score 489.5; DB 2; 27.9%; Pred. No. 1.8e-22; iive 50; Mismatches 202;
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                       Query Match
Best Local Similarity 27.99
Matches 193; Conservative
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                                                                                                                         A;Cross-references: UNIPROT: Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
A;Note: sequence extracted from NCBI backbone (NCBIP:127318)
R;Franco del Amo, F.; Smith, D.E.; Sviatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
Bubmitted to the EMBL Data Library, April 1992
A;Description: Expression pattern of Motch, a mouse homolog of Drosophila Notch, suggest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: nucieic acid
A;Residues: 1865-1932, 'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054
A;Residues: 1865-1932, 'RR',1935-1937,'L',1938-1967,'I',1969-2044,'IE',2047-2052,'S',2054
A;Rexperimental Bource: embryo
A;Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)
C;Comment: This protein has many EGF repeats and lin-12[#1172]/Notch repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
A;Reference number: A46438; MUID:93252998; PMID:8486742
A;Accession: B46438
                                                                                                                                                                                                                                                                           A;Accession: S25144
A;Molecule type: mRNA
A;Crose-references: EMBL:Z11886
B;Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A;Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety
A;Reference number: A49175; MUID:93178563; PMID:8440332
A;Accession: C49175
A;Accession: C49175
A;Statuus: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1161-1547 < LAR>
A;Acrose-references: EMBL:X68278; NID:9287987; PIDN:CAA48339.1; PID:9287988
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rotein; ankyrin repeat homology; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Note: sequence extracted from NCBI backbone (NCBIP:126159) R;Kopan, R.; Weintraub, H. J. Cell Biol. 121, 631-641, 1993
A;Reference number: A46019; MUID:93194170; PMID:8449489
A;Accession: A46019
                                                                A;Status: not compared with conceptual translation A;Molecule type: nucleic acid
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EGF homology «EG16»
EGF homology «EG18»
EGF homology «EG18»
EGF homology «EG18»
EGF homology «EG19»
EGF homology «EG19»
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F;2016-2048/Domain:
F;2049-2081/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:987-1018/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1149-1180/Domain:
                                                                                                                  A; Residues: 1-2531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;106-138/Domain:
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A; Note: proximal 1
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Search completed: November 29, 2004, 13:27:05 Job time : 17.4855 secs
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                                                                                                                                                                                                                                                              DLTENPERLISRLTQRHLVGEEWSQDLHSSGRTDLYSYRFVCDEHYYGEGCSV----FC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYTG--CE---EEC---PCKN-GSCTDLESS--CTCPPGFYG-KCELSAMTCADGPCFNG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRC-------CPLG-SGFN 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908 NIDE-----CAGGPHCLNGGQCVDRIGGYTCRCLPGFAGERCEGDINECLSNPCSSE- 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
$18188
c) Control protein homolog - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-Fb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C;Accession: S18189
R;Weinmaster, G; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
                                                                                                                                                                          CENDÉRCIDL----VNGYQCNCQPGTSGLNCEINFDDCASNPCWHGVCVDGINRYSCVCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCRGGGCCTFFRVCLKHYQASVSP-----SPPCTYGSATPVLGSF---S
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                                                                                                                                                                                                                                                                                                                                                                                             505 MLPYTGKNCQTVLAPCSPNPCENAAVCKEAPNFESFSCLCAPGWGCKRCTVDVDECISKP
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                                                                                                                                59; Mismatches 178; Indels 310;
    ankyrin repeat homology; EGF homology
                                                                                                         Length 1203;
                                                                                                                                                                                                                                                                                                                 168 RPRDDFGHFTCG---RGEKC---PGWKGQYC------
                                                                                                        14.3%; Score 485; DB 2; 25.2%; Pred. No. 1.9e-22;
C;Superfamily: Notch protein; ankyrin F;143-174/Domain: EGF homology <EGX1>F;482-513/Domain: EGF homology <EGF>F;560-591/Domain: EGF homology <EGF>F;674-705/Domain: EGF homology <EGX>F;712-743/Domain: EGF homology <EGX>F;836-867/Domain: EGF homology <EGX3>F;836-867/Domain: EGF homology
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                                                                                                     Query Match
Best Local Similarity 25.2*
Matches 184; Conservative
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A;Title: A homolog of Drosophila Notch expressed during mammalian development. A;Reference number: $18188; MUID:92111383; PMID:1764995
A;Recession: $18188
A;Molecule type: mRNA
A;Residues: 1-2531 <WEI>
A;Cross-references: BMBL:X57405; NID:957634; PID:957635
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology
F;1025-1056/Domain: EGF homology <EGF>
F;1023-1056/Domain: EGF homology <EGF>
F;1033-1264/Domain: ankyrin repeat homology <ANI>
F;1984-2016/Domain: ankyrin repeat homology <ANI>
F;1984-2016/Domain: ankyrin repeat homology <ANI>
F;2017-2049/Domain: ankyrin repeat homolog
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.larity 27.5%; Pred. No. 3.7e-22;
Conservative 52; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1120 GLCVDEEDKHYCHCQAGYTGSYCEDEVD 1147
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Best Local Similarity
Matches 189; Conserv
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Q90656 gallus gall
Q61483 mus musculu
Aah57400 mus musculu
Aah57603 mus muscul
Aar20869 mus muscul
Aar5063 mus muscul
Aar5063 mus muscul
Aar5063 mus muscul
Q01502 rattus norv
Q00548 homo sapien
Q8aw37 cynops pyrr
Q91922 xenopus lae
Q81357 brachydanio
Q6448 brachydanio
Q6448 brachydanio
Q6448 brachydanio
Q57xt4 xenopus lae
Q73xt4 xenopus lae
Q73xt4 xenopus lae
Q6448 cupienius
Q6448 cupienius
P10041 drosophila
Q6t4n1 drosophila
                                                                         November 29, 2004, 13:12:09; Search time 69.5872 Seconds (without alignments) 4779.132 Million cell updates/sec
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                                                                                                                                     3383
1 MGRLLASALLCVSGVFELKL......DTKYQSVYVSEKDECIATEV 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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AAR30869
AAH65063
DLL1_RAT
DLL1_HUMAN
QBAW87
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DLL4 MOUSE
Q9DBÜ9
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Maximum Match 100%
Listing first 45 summaries
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DLL1_MOUSE
                                                      - protein search, using sw model
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DL_DROME
Q6T4M9
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Q6D148
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Q7ZXT4
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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32 1086.5 32.1 833 2 AAR21453 Aar21453 drosophil 34 1086.5 32.1 833 2 AAR21454 Aar21454 drosophil 35 1086.5 32.1 833 2 AAR21455 Aar21456 drosophil 36 1086.5 32.1 833 2 AAR21456 Aar21456 drosophil 37 1086.5 32.1 833 2 AAR21459 Aar21459 drosophil 39 1086.5 32.1 833 2 AAR21461 Aar21459 drosophil 40 1086.5 32.1 833 2 AAR21461 Aar21460 drosophil 41 1086.5 32.1 833 2 AAR21462 Aar21461 drosophil 42 1086.5 32.1 833 2 AAR21462 Aar21464 drosophil 44 1086.5 32.1 833 2 AAR21465 Aar21465 drosophil 44 1086.5 32.1 833 2 AAR21466 Aar21466 drosophil 45 1086.5 32.1 833 2 AAR21465 Aar21466 drosophil 45 1086.5 32.1 833 2 AAR21466 Aar21466 drosophil 45 1086.5 32.1 833 2 AAR21466 Aar21466 drosophil
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ALIGNMENTS

26.54	SULT 1 09656 096656 01-NOV-1996 (TTEMBLEAL) 10-NOV-1996 (TTEMBLEAL) 11-NOV-1996 (TTEMBLEAL) 12-NOV-1996 (TTEMBLEAL) 13-NOV-1996 (TTEMBLEAL)	ជា ការារា ០.		28 AA. nce up ation ; vert rmes; IEA. IEA. 66D238	Euteleostomi; dae; Phasianinae; Ish-Horowicz D.; ons in the in th
Σ	Matches 546;	Conservative	9; Mism	Mismatches 19;	Indels 144; Gaps 65;
ò	5 LAS	LASALLCVSGVFBLKLQEFVNKKGLL-NRNCCRGGG	KLOEFVNKI	KGLL-NRNCCRGG	G
qq	11 LLS	ALLCRCQVDGSGVFEL	KLOEFVNKI	KGLLSNRNCCRGG	11 LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQCDCKTFFRVCL 70

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium-binding (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calcium-binding (Potential)
heart and at lower levels, in adult lung.
-!- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.
Expression then decreases and increases again in the adult.
-!- SIMILARITY: Contains 1 DSL domain.
-!- SIMILARITY: Contains 8 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Delta-like protein 1.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential.
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4. cal
EGF-like 5.
EGF-like 6.
EGF-like 7. cal
EGF-like 8.
EGF-like 8.
EGF-like 9.
EGF-like 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
                                                                                                                                                                                                                                    EMBL; X80903; CAA56865.1; -. PIR; 148324; 148324.
HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IntAct; Q61483; -. MGD; MGI:104659; D111.
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SIGNAL 1
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130
                                                                   103 IEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHY 158
                                                                                                     190
                                                                                                                                                                                                         KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGAT 270
                                                                                                                                                                                                                         CINTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
                                                                                                                                                                                                                                                                                             CTNTGQGSYTCSCRPGYTGSSCELEINECDANPCKNGGSCTDLENSYSCTCPPGFYGKNC 370
                                                                                                                                                                                                                                                                                                                                             ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CVDL 369
                                                                                                                                                                                                                                                                                                                                                               GNSY-C-COAGF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                    GNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCPPGYNGKNCSTPVS 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPP-GPV------DEEQ 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPW-AVCAGLVL---LLLGCAA-VVCVRLK-----QKPEC---ETETMNNLANCQREKD- 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --SSIGATQIKNTNKK-DFH----DK---KVRYP-VDYNLVLKV------HKKC--- 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 SISVIGATQIKNTNKKVDFHSDNSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAK 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SEEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHYQASVSPEPPCTYGSA-TPVLG--SFS-PDGAG--DPAFSNPIRFPFGFTWPGTFSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE SEL/6 X BALB/c; TISSUE=Embryo;
MEDLINE=95401858; PubMed=7671806;
Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
"Transient and restricted expression during mouse embryogenesis of
"Transient and restricted expression during mouse embryogenesis of
D111, a murine gene closely related to Drosophila Delta.";
Development 121:2407-2418(1995).
                   KHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGFTWPGTFSLI
                                                                                     131 IEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSYRFVCDEHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
Deltarlike protein 1 precursor (Drosophila Delta homolog 1) (Delta1)
Mume=Dll1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system. SUBUNIT: Interacts with Notch receptors.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: In the embryo, expressed in the paraxial mesoderm and nervous system. Expressed at high levels in adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                       251
                                                                                                                                                                                                                                                                                                           311
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STRAIN=C57BL/6J;
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                                                                                                                                                                                                              Delta-like 1.
                                                                                                                                                                                                                                      Name=Dlll
                                                                                   · Q6PFV7
                                RESULT 3
Q6PFV7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIIEALHTDSPDDL-TENPERLISRL-TORHL-VGEEWSQDLHSSGRTDL-YSYRPVCDE 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCINIGOGSYICSCRPGYIG -- CE---EEC---PCKNG-SCIDLES--SCICPPGFYGK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLGNSY-C-COAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2466; DB 1;
Pred. No. 3.5e-172;
6; Mismatches 19;
                          similarity.
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By similarity.
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  II 722
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DISULPID
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A KIAINELO FALLO STATE STORE THE STATE STA
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 7015_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AY497019; AAR30869.1; -. GO: 0005515; F: protein binding; IPI.
GO: GO: 0005515; F: protein binding; IPI.
GO: GO: 0007386; P: compartment specification; IMP.
GO: GO: 0007386; P: determination of left/right symmetry; IMP.
GO: GO: 0001757; P: somite specification; IMP.
InterPro; IRR000152; AR. Aydroxyl_S.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains B EGF-like domains.
EMBL; BCO57400; AAHS7400.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                   Created)
Last sequence update)
Last annotation update)
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722 AA
PRT;
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... IPR001438; EGF II.
... IPR006209; EGF II.
InterPro; IPR006210; IEGF.
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
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STRAIN=C57BL/6; TISSUE=Mouse;
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STRAIN=C57BL/6; TISSUE=Mouse;
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PRELIMINARY;
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05-JUL-2004 (TrEMBLrel.
01-OCT-2004 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSGRTDLRYSYRFVCDE 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFYGK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCTNTGQGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGK 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 VCELSAMICADGPCFNGGRCSDNPDGGYICHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCOFLLPE-PPGP--VD-----EEQ- 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK---PE-C--ETETMNNLANCQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYYGEGCSVFCRPRDDAFGHFTCGDRGEKMCDPGWKGQYCTDPICLPGCDDQHGYCDKPG
                                                                                                                                                                                                                                                                                                                          -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKKD--C-SSPC-NGA-CV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------CSEEKAL------RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IAT
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                      19; Indels 144;
                                                                                                                                                                                                                                          Length 722;
                                                                                                                                                                                                                                                                                                       MGR-----LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGG
                                                                                                                                                                                                             9D570B9DC7EEC75E CRC64;
                                                                                                                                                                                                                                       Score 2466; DB 2;
Pred. No. 3.5e-172;
6; Mismatches 19;
Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 6.
Pfam; PF0745; EGF CA; 1.
PRINTS; PR0010; EGFBLOOD.
SWART; SW0010; EGFBLOOD.
SWART; SW00119; EGF; 8.
SWART; SW00119; EGF, 8.
PROSITE; PS00110; ASK HYDROXYL; 3.
PROSITE; PS0012; EGF_1; 8.
PROSITE; PS0126; EGF_1; 8.
PROSITE; PS0126; EGF_1; 8.
PROSITE; PS01187; EGF_2; 8.
PROSITE; PS01187; EGF_1; 8.
PROSITE; PS01187; EGF_1; 8.
PROSITE; PS01187; EGF_1; 8.
PROSITE; PS01187; EGF_1; 8.
                                                                                                                                                                                                           722 AA; 78449 MW;
                                                                                                                                                                                                                                       Match 72.9%;
Local Similarity 76.6%;
les 553; Conservative
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SEQUENCE FROM N.A.

REGUENCE FROM N.A.

STAIN=CS7BL/6; TISSUE=Mouse;

RX MISDINE=2138825; PubMed=12477932;

RIA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Noriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human RT and mouse CDNA sequences.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS
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                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057400; AAH57400.1; -
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                 Created)
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STRAIN-C57BL/6; TISSUE-Mouse;
AAH57400 PRELIMINARY;
AAH57400;
O2-MAR-2004 (TrEMBLrel. 2'
02-MAR-2004 (TrEMBLrel. 2'
02-MAR-2004 (TrEMBLrel. 2'
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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STRAIN-CSTRUK, N.T.

SUCHANDE TROWN N.T.

STRAIN-CSTRUK, N.T.

WEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Teingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raphey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nodriguez A.C., Marram M.A.,

Johns S.J., Marram M.A.,

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGRNCSAP 480
                                                     ATCTNITGGGSYTCSCRPGYTGANCELEVDECAPSPCKNGASCTDLEDSFSCTCPPGFYGK
                                                                                                                                                                                                                                                       VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV
                            ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCINICOGSYTCSCRPGYIG--CE---EEC---PCKNG-SCIDLES--SCICPPGFYGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27,
02-MAR-2004 (TrEMBLrel. 27,
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361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV 420
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                                                                            DIGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP
                                                                                                                                                                                  VSRCEHAPCHNGATCHQRQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG
                                              DLGNSY-C-CQAGP-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P
                                                                                                                                                    -----BEO-
                                                                                                                                                                                                                                                --FPW-AVCAGIV---LLLLLGCAA-VVCVRLK-OK----PE-C--ETETMNNLANCOREK
                                                                                                                                                                                                                                                                       GPFPWVAVCAGVVLVLLLLGCAAVVVCVRLKLQKHQPPPEPCGGETETMINLANCQREK
                                                                                                                                                                                                                                                                                                                                              D---SSIGATQIKNTNKK-DFHDK------KVRYP-VDYNLV--LK-----VHKK
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Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                               VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nagaraja R., Waeltz P., Brathwaite M.E.; "Genomic Sequence Analysis in the Mouse t-complex Region."; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY497019; AAR30069.1; -
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 72.9%; Score 2466; DB 2; I sal Similarity 76.6%; Pred. No. 3.5e-172; 553; Conservative 6; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       722
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Mammalia; Eutheria; Rodentia;
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AAR30869,
02-MAR-2004 (TrEMBLrel. 2
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R GO; GO:0005576; C:attracellular; ISS.

RG; GO:0005576; C:integral to plasma membrane; ISS.

RG; GO:0005512; F:notch binding; IPI.

RG; GO:00030154; P:cell differentiation; ISS.

RG; GO:0001701; P:embryonic development (sensu Mammalia); ISS.

RG; GO:0001701; P:embryonic development (sensu Mammalia); ISS.

RG; GO:0001701; P:hemopoiesis; ISS.

RG; GO:00043472; P:hemopoiesis; ISS.

RG; GO:00043472; P:nourcgenesis; ISS.

RG; GO:0007219; P:nourcgenesis; ISS.

RG; GO:0007219; P:nourcgenesis; RSS.

RG; GO:0007219; P:nourcgenesis; RSS.

RG; GO:0007219; P:nourcgenesis; RSS.

RG; GO:0004375; P:regulation of cell adhesion; ISS.

RG; GO:0004375; P:regulation of cell adhesion; ISS.

RICEPPO; IPRO0125; Asx hydroxyl_S.

RICEPPO; IPRO0125; BGF_2.

RICEPPO; IPRO01475; EGF_2.

RICEPPO; IPRO0148; EGF_2.

RICEPPO; IPRO01491; EGF_2.

RICEPPO; IPRO01491; EGF_1.

RICEPPO; IPRO01491; EGF_1.

RICEPPO; IPRO01491; EGF_1.

RICEPPO; IPRO01491; EGF_1.

RICEPPO; RRO0101; EGF_1.

REAM; PRO0115; EGF_1.

REAM; PRO0115; EGF_1.

REAM; PRO0115; EGF_1.

REAM; REAM; REAMOOS1; EGF_1.

REAM; REAM; REAM; REAMOOS1; EGF_1.

REAM; REAM;
                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           SEQUENCE FROM N.A.
Distblo G., Hebbhi L., Boulter J., Weinmaster G.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May be involved in cell-to-cell communication in mammalian embryos. May have a role in cellular interactions underlying somitogenesis and development of the nervous system (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EGF-like 1.
EGF-like 2.
EGF-like 3.
EGF-like 4, calcium-binding (Potential).
EGF-like 5.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delta-like protein 1.
Extracellular (Potential)
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                                                                                                                                                                                                                                              similarity).
--- SUBUNIT: Interacts with Notch receptors.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SIMILARITY: Contains 1 DSL domain.
--- SIMILARITY: Contains 8 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential
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                                     Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                61 VCLKHYQASVSPEPPCTYGSAVTPVLGVDSFSLPDGAGIDPAFSNPIRFPFGFTWPGTFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                               121 LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 HYYGEGCSVPCRPRDDAFGHFTCGDRGEKKCDPGWKGQYCTDPICLPGCDDQHGYCDKPG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKNG-SCTDLES--SCTCPPGFYGK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ATCTNIGGGSYICSCRPGYIGANCELEVDECAPSPCKNGASCIDLEDSFSCICPPGFYGK 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPLGFSGFNCEKKMDLCGSSPCSNGAKCV 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 DLGNSYLCRCQAGFSGRYCEDNVDDCASSPCANGGTCRDSVNDFSCTCPPGYTGKNCSAP 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ- 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 VSRCEHAPCHNGATCHQRGQRYMCECAQGYGGPNCQFLLPEPPPGPMVVDLSERHMESQG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FPW-AVCAGLV---LLLLGCAA-VVCVRLK-QK----PE-C--ETETMNNLANCQREK 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 GPFPWVĄVCAGVVLVLLLLLGCAAVVVCVRLKLQKHQPPPBFCGGETETMNNLANCQREK 600
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                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                          19; Indels 144;
                                                                                                                                                                       Length 722;
                                                               Strongerg R.;
Strongerg R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC065063; AAH65063.1; -.
SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                     72.9%; Score 2466; DB 2; 76.6%; Pred. No. 3.5e-172; tive 6; Mismatches 19;
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Last sequence update)
Last annotation update)
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             [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Mouse;
                                                                                                                                                                                                          Matches 553; Conservative
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                                                                                                                                                                                         Similarity
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05-JUL-2004
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DLL1_RAT
ID DLL1_RAT
AC P0767;
DT 01-NOV-199
DT 01-NOV-199
DT 05-JUL-200
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Exp. Med. 194:991-1001 (2001).
FUNCTION: Acts as a ligand for Notch receptors. Blocks the differentiation of progenitor cells into the B-cell lineage while promoting the emergence of a population of cells with the characteristics of a T-cell precursor.
SUBUNIT: Interacts with Notch receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21464863; PubMed=11581320;
Jaleco A.C., Neves H., Hooijberg B., Gameiro P., Clode N., Haury M.,
Henrique D., Parreira L.;
"Differential effects of Notch ligands Delta-1 and Jagged-1 in human
lymphoid differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bloinformatics assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-2288726; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chan B., Crwoley C., Currell B., Deuel B., Dowd P. Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lee J., Lao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura A., Yi S., Yu G., Yuan J., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Micsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas :
"Human ligands of the Nocch receptor.";
Am. J. Pathol. 154:785-794(1999).
                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                                                       GSVGEEKSISTLRGGEVPDRKRPESVYSISKDTKYQSVYVLSAEKDECVIATEV
                                                                     RKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Han W., Ye Q., Moore M.A.S.;
A soluble form of human delta-like-1 inhibits differentiation hematopoidetic progenitor cells.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                        000548; Q9NU41; Q9UJV2;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2014 (Rel. 1 precursor (brosophila Delta homolog 1)
(H-Delta-1) (UNQ146/PRO172).
                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oda T., Chandrasekharappa S.C.;
"Human Delta 1 gene sequence.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                        723
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                     ---SEEKAL----
                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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[2]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A
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Godowski P.;
                                                                                                                                                                                                        DLL1_HUMAN
                                                                                                                                                                                                                                                                                                                                             Name=DLL1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTINTGOGSYTCSCRPGYTG--CE---BEC---PCKN-GSCTDLES--SCTCPPGFYGK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK---DCSSPC-NGA-CV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCELSAMTCADGPCFNGGRCSDNPDGGYTCHCPAGFSGFNCEKKIDLCSSSPCSNGAKCV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLGNSY-C-CQAGF-GR-C-DNVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-P 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSRCEH-PCHNGATCHRR----YCECA-GYGG-NCQFLLPEPPGPV----DEEQFPW-AV 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGLV---LLLLGCAA-VVCVRLK----QKP--EC--ETETMNNLANCQREKD---SSIG 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600
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EGF-like 7, calcium-binding (Potential).

EGF-like 8.

B similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIIEALHTDSPDDLATENPERLISRLTTQRHLTVGEEWSQDLHSSGRTDLRYSYRFVCDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYYGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGC-DQHG-CDKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -linked (GlcNAc. . .) (Potential).
4B8EE2272BAEA27E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.0%; Score 2436; DB 1; Length 714; 75.4%; Pred. No. 5.4e-170; ive 11; Mismatches 29; Indels 13:
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      714 AA;
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DDLATENPERLISRLATQRHLTVGEEWSQDLHSSGRTDLKYSYRFVCDEHYYGEGCSVFC 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCSCRPGYTG--CE---BEC---PCKN-GSCTDLES--SCTCPPGFYGK-CELSAMTCAD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEPPCTYGSA-TPVLG--SPS-PDGAG-DPAFSNPIRFPFGFTWPGTFSLIIEALHTDSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATCHRR----YCECA-GYGG-NCQFLLPE-PPGP--VD-----EEQ---FPW-AVCAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 YCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCRNGATCTNTGQGSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDL-TENPERLISRL-TORHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFC
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                                                                                                                                                                                                                                                                                                                                                                                                        . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.0%; Score 2401.5; DB 1; Length 723; 75.1%; Pred. No. 1.8e-167; Indels 139; ive 11; Mismatches 27; Indels 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> S (1D Ref. 2).
B4EC455FFA32A12B CRC64;
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-> R (in Ref. 4 and 5).
-> S (in Ref. 2).
By similarity.
By sim
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Matches 534; Conservative
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R. GO; GO:000587; C:extracellular; NAS.

R. GO; GO:0005887; C:integral to plasma membrane; NAS.

R. GO; GO:000512; F:Notch binding; IPI;

R. GO; GO:0001701; F:Notch binding; IPI;

R. GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.

R. GO; GO:0001701; P:hemopoiesis; NAS.

R. GO; GO:0001701; P:hemopoiesis; NAS.

R. GO; GO:0001701; P:hemopoiesis; NAS.

R. GO; GO:0007219; P:hemopoiesis; ISS.

R. GO; GO:0007219; P:nourogenesis; ISS.

R. GO; GO:0007219; P:nourogenesis; ISS.

R. GO; GO:0007219; P:regulation of cell adhesion; TAS.

R. InterPro; IPR00143; EGF_2.

R. InterPro; IPR00143; EGF_2.

R. InterPro; IPR00143; EGF_1.

R. InterPro; IPR00143; EGF_1.

R. REAM; PF00144; DSL; I.

R. REPRO; REPRO010; BGF_11;

R. REAM; PR00117; BGF_2.

R. REAM; PR00117; BGF_2.

R. REAM; PR00119; EGF_2; B.

R. RROSITE; PS001186; EGF_2; B.

R. RROSITE; PS001186; EGF_2; B.

R. RROSITE; PS001186; EGF_2; B.

R. RROSITE; PS001187; EGF_2; I.

R. RROSITE; PS001187; EGF_2; I.

R. RROSITE; PS01187; EGF_CA; I.

R
                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BGF-like 1.
BGF-like 2.
BGF-like 3.
BGF-like 4, calcium-binding (Potential).
BGF-like 5.
BGF-like 6.
BGF-like 6.
BGF-like 7, calcium-binding (Potential).
BGF-like 7, BGF-like 7, BF-like 8.
BGF-like 9.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower expression in brain and muscle and almost no expression in placenta, lung, liver, and kidney.
SIMILARITY: Contains 1 DSL domain.
SIMILARITY: Contains 8 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delta-like protein 1.
Extracellular (Potential).
Potential.
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                                                                                                                                                                                                                                                                                                                                   EMBL, AF003522; AAB61286.1; --
EMBL, AF196571; AAF0834.1; --
EMBL, AY328392; AAG9716.1; --
EMBL, AX368992; AAG8251.1; --
EMBL, AL078605; CAB89569.1; --
HSSP, P00740; 1EDM.
Genew, HGNC:2908; DLL1.
MIM, 606582; --
GO; GO:0005576; C:extracellular;
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SIGNAL 1
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    CINTGQGSYTCSCRPGYTGANCEIEVNECEASPCKNGGSCADLENSYSCSCPPGFYGKNC 366
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                                                                                                                                                                                                                                                                                                                                                                         ---SSIGATQIKNTNKK-----DFHDKKVRYP-VDYNLVL------KVH 538
                                                                                                                                                                                                                                                                                                                                                                                                  607 ISVSVIGATQIKNTNKKADLYSESTSDKNGYKARYPSVDYNLVHELKHEDSVKEEHGKRE 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNSYCCQA--GF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVS
                                                                                                                                                              GNSYICQCLDGFSGRHCDDNLDDCASYPCANGGTCQDGVNDYSCTCPPGYNGKNCSTPVS
                                                                                                                                                                                                                                                                                                                   ELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSS-PC-NGA-CVDL
                                                                                                                                                                                                                 RCEH-PCHNGATCHRR----YCECA-GYGG-NCOFLLPEPPGPVDE------EQ
                                                                                                                                                                                                                                           FPW-AVCAGLVL---LLLGCAA-VVCVRLKQKPE-----CETETMNNLANCQREKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95319507; PubMed=7596411;
Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowicz
"Expression of a Delta homologue in prospective neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           721 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; F:calcium ion binding; IEA.
GO; GO:0005154; P:calcium ion binding; IEA.
INCEPTO; IPR000152; ASX. hydroxyl_S.
INCEPTO; IPR000174; DSL.
INCEPTO; IPR000142; EGF_2.
INCEPTO; IPR001841; EGF_Ca.
INCEPTO; IPR001843; EGF_II.
INCEPTO; IPR001841; EGF_Ca.
PFam; PF01414; DSL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
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SMART; SM0005; DSL; 1.
SMART; SM0109; EGF_CA; 4.
PROSITE; PS00010; ASX HYPROXYL;
PROSITE; PS00022; EGF_1; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEALHTDSPDDL-TENPERLISRLT-ORHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGEGCSVFCRPRDD-FGHFTCG-RGEK-C-PGWKGQYCT-PICLPGCD-QHG-CDKPGEC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLPCNQDLNYCTHHKPC-NGAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-C 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                     Cynops pyrrhogaster (Japanese common newt).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
NCBI_TaxID=8330;
Query Match 67.0%; Score 2267.5; DB 2; Length 726; Best Local Similarity 68.9%; Pred. No. 1.2e-157; Matches 496; Conservative 23; Mismatches 56; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LLASALLCV----SGVFELKLQEFVNKKGLL-NRNCCRGGG----
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
Submitred (OCT-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 8 EGF-11ke domains.
EMBL; AB095017; BAC41350.2;
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                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR.2003 (TrEMBLrel. 23, 01-MAR.2004 (TrEMBLrel. 26, 01-MAR.2004 (TrEMBLrel. 26, Ligand Delta-1.
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
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241 CKCRVGFSGKYCDDCIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPCQNGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 VCLKHYQASVSPEPPCTYGSA-TPVLGSFS---PDGAGDPAFSNPIRFPFGFTWPGTFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYGEGCSVFCRPRDD-FGHFTCG-RGE-KC-PGWKGQYCT-PICLPGCDQ-HG-CDKPGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGA
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                                                                                             zebrafish deltaD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.6%; Score 2084.5; DB 2; Length 720; 63.4%; Pred. No. 3e-144; ive 51; Mismatches 69; Indels 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 SRCEH-PCHNGATCH----RRYCEC-AGYGG-NCOFLLPE-PPGPV----
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                           MEDLINE=22248969; PubMed=12361969;
Hans S., Campos-Ortega J.A.;
"On the organisation of the regulatory region
                                                                                                                                                                                    EMBL; AFG26384; AAL315281; EMBL; AFG26384; AAL315281; EMBL; AFG26384; AAL315281; EMBL; AFG26384; AAL315281; E. HSSP; P00740; IEDM.
GO; GO:0016200; C:membrane; IEA.
GO; GO:0007154; P:calcium ion binding; IEA.
GO; GO:0007154; P:calcium ion binding; IEA.
InterPro; IPR001152; Asx. hydroxyl_S.
InterPro; IPR00174; DSL.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_II.
SPR00181; EGF_CA:
FF AMBL; SM00179; EGF_CA: 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROXYL; 3.
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R PROSITE; PS00010; ASX HYDROXYI
R PROSITE; PS01186; EGF_1; 8.
PROSITE; PS01186; EGF_2; 8.
PROSITE; PS01187; EGF_2; 8.
PROSITE; PS01187; EGF_CA; 2.
EGF-like domain.
SEQUENCE 720 AA:
                                                                                                                                   gene.";
Development 129:4773-4784(2002)
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Matches 456; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGFNCEKK--DCSS-PC-NGA-CVDLGNSY 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATQIKNTNKK-DF-----HDKKVRYP-VDYNLV------LKVHKKCS--- 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 QASVSPEPPCTYGSA-TPVLGSFS---PDGA-GDPAFSNPIRFPFGFTWPGTFSLIIEAL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGIVLVLMLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMNNLANCQREKDISVSFIG 609
                                                                                                                                                                                                                                                                                                                                                                                                    69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SUPECRPROD-FGHFTGG-RGEK-C-PGWKGQYCT-PICLPGCDQHG--CDKPGECKCRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 CSDYCRPRDDAFGHFSCGEKGEKLCNPGWKGLYCTEPICLPGCDEHHGYCDKPGECKCRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 CCQA--GF-GR-C-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNCS-PVSRCEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 ICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCPPGYIGKNCSMPITKCEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 NPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPEEKPVVVDLTEKYTEGQSGQFPWIAV
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                                                                                                                                                                                                                                                                                                                                                                            10 LVLSAVLCQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSLASLQRCECKTFFRICLKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLESS--CTCPPGFYGK-CELSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              422 -PCHNGATCHRR----YCECA-GYGG-NCQFLLP-EPPGFVD------EEQFPW-AV
                                                                                                                                                                                                                                                                                                                                         4 LLASALLC---VSGVFELKLQEFVNKKGLL-NRNCCRGGG------CCTFFRVCLKHY
                                                                                                                                                                                                                                                                       Gaps
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;

Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cypriniformes;

Cyprinidae; Danio.

(VCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         670 SDSEDVNSVHSKRDSBERRRPDSAYSTSKDTKYQSVYVISDEKDECIIATEV 721
                                                                                                                                                                                              66.9%; Score 2262.5; DB 2; Length 721; 68.7%; Pred. No. 2.8e-157; inve 39; Mismatches 47; Indels 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- EEKALRKRP-SVYSTSKDTKYQSVYV--SEKDEC-IATEV
                                                                                                                                721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DeltaD protein.
PS01186; EGF_2; 8.
PS50026; EGF_3; 6.
PS01187; EGF_CA; 2.
                                                                                                                                                                                                                                    Best Local Similarity 68.7%
Matches 489; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
PROSITE; PS01186;
PROSITE; PS50026;
PROSITE; PS01187;
EGF-like domain.
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                                                                                                                                   SEQUENCE
                                                                                                                                                                                                         Query Match
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AC Q80W0
DT 01-MA
DT 01-MA
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DT 01-MA
DT 02-MA
DT 02-MA
DT 02-MA
DT 03-MA
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TISSUBEENEVE;

TISSUBSENEVE;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MAISCANI S. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.P., Zoeberg B. Buetcw K.H., Schaefer C.F., Bhate N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haidh F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcinci P. Prange C., Nack S., Worley K.C., Hale S., Garcinci B. H., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Akaseley R.W., Touchman J.W., Green B.D., Dickson M.C., Akaseley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Ab. Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYGEGCSVFCRPRDDTFGHFTCGERGEIICNSGWKGQYCTEPICLPGCDEDHGFCDKPGE
                                                                                            rcinigosyrcscrpdfigoscelevaecsgspcrngscrplentyscrcppgfygrn
                                                                                                                                                                                                                                             CELSAMTCADGPCFNGGHCADNPEGGYFCQCPMGYAGFNCEKKIDHCSSNPCSNDAQCLD
                                                                                                                                                                                                                                                                                                                      : ||| |||||::|:|| | |::|| | DGGFPWIAVCAGIILVILVILGGSVFVIYIRLKLQQRSQQIDSHSEIETWANLTNNRSRE
                                                                         CKCRVGWQGRYCDECIRYPGCVHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGA
                                                                                                                                                                                                                                                                                                 LGNSYCCQAGFG----RC-DNVDDCAS-PC-NGGTCD--VND-SCTCPPGY-GKNC-SPV
                                                                                                                                                                                                                                                                                                                                                                        417 SRCEH-PCHNGATCH----RRYCEC-AGYGG-NCQFLLPE-PPGPV-----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BEOFPW-AVCAGLVLLLL----GCAAVVCVRLKQK------PECETETMNNLANCQ-RE
   YYGEGCSVFCRPRDD-FGHFTCG-RGE-KC-PGWKGQYCT-PICLPGCDQ-HG-CDKPGE
                                                                                                                                                    TCTNTGQGSYTCSCRPGYTG--CE---EEC---PCKN-GSCTDLES--SCTCPPGFYGK-
                                                                                                                                                                                                                         CELSAMTCADGPCFNGGRC-DNPDGGY-C-CPLG-SGPNCBKK--DCSS-PC--NGACVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KC-----SEEK-----ALRKRPSVYSTSKDTKYQSVYV--SEKDEC-IATEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 ATKCEPLDSDSEEKHRNHLKSDSSERKRTE--SLCKDTKYOSVFVLSEEKDECIIATEV
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KD---SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVLKVHK-----
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
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NCBI_TaxID=7955;
                                      181
                                                                         211
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Q6D148;
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                                  601 KDLSVSIIGATQVKNINKKVDPQSDGDKNGFKSRYSLVDYNLVHELKQEDLGKEDSERSE 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ICLKHYQANVSPDPPCTYGGAVTPVLGSNSFQVPESFPDSSFTNPIPFAFGFTWPGTFSL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 IIEALHTDSTDDLSTENPDRLISRMTTQRHLIVGEEWSQDLQVGGRTELKYSYRFVCDEH 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEH 157
                                                                                            1 MGRLMIAVLLCVMISQGFCSGVFELKLQEFLNKKGVTGNANCCKGSAAEGHQCECKTFFR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 VCLKHYQASVSPEPPCTYGSA-TPVLGSFS---PDGAGDPAFSNPIRFPFGFTWPGTFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurogenic
somitic
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                                                                         --KC-----SEEK-----ALRKRPSVYSTSKDTKYQSVYV--SEKDEC-IATEV
                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae, Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dornseifer P., Takke C., Campos-Ortega J.A.; "Overexpression of a zebrafish homologue of the Drosophila gene delta perturbs differentiation of primary neurons and
KD---SSIGATQIKNTNKK-DFH---DK---KVRYP-VDYNLVLKVHK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9C5A0162504593E4 CRC64;
                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.5%; Score 2081.5; DB 2;
63.4%; Pred. No. 5e-144;
iive 51; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. (3.159-171 (1997).

BMBL; Y1760; CAA72425.1; -.

HSSP; POOT40; LEDM.

ZFIN; ZDB-GENE-990415-47; dld.

GO; GO:0005509; F:caLclum ion binding; LEA.

GO; GO:000754; F:caLclum ion binding; LEA.

GO; GO:0007154; F:caLlum ion binding; LEA.

GO; GO:0007154; F:caLlum ion binding; LEA.

InterPro; IPR000152; Asx_hydroxyl_S.

InterPro; IPR000152; Asx_hydroxyl_S.

InterPro; IPR0001474; DEL.

InterPro; IPR000143; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR001639; EGF_II.

InterPro; IPR001639; EGF_II.

Pfam; PP01414; DSL; 1.

Pfam; PP001019; EGF_LOS.

SMART; SM00051; DSL; 1.
                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequenc
01-MAR-2004 (TrEMBLrel. 26, Last annotat
elablad transmembrane protein precursor.
Name-dld; Synonyms-deltab;
Brachydanio rerio (Zebrafish) (Danio rer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01187; EGF_CA; 2.
EGF-like domain; Signal; Transmembrane.
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01-MAR-2004 (
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                                                                                                                                                                                                                                   TFFRVCLKHYQASVSPEPPCTY-GSATPVLGSFS----PDGAGDPAFSNPIRFPFGFTWPG
                                                                                                                                                                                                                                                                                  TFSLIIEALHTDSPDDL-TENPERLISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -CVDLGNSYCCOAGFG----RCDNV-DDCAS-PC-NGGTCDVNDS---CTCPPGY-GKNC
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                                                                                                                                                            Gaps
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                                                                                                                                   Similarity 58.4%; Score 2014; DB 2; Length 772; Similarity 58.4%; Pred. No. 4.8e-139; Conservative 48; Mismatches 76; Indels 198;
                                                TISSUE=Embryo;
Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ database:
EMBL, BCO75742, AAH75742.1; -.
Hypothetical protein.
SEQUENCE 772 AA; 84968 WW; 716A014158938576 CRC64;
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LKVHKKCSEEKALRKR
                         [2]
SEQUENCE FROM N.A.
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                                                                                                                                                           Matches 452;
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O57462 PRELIMINARY; PRT; O57462; O1-JUN-1998 (TrEMBLrel. 06, Created)

RESULT 14 057462 ID 05746 AC 05746 DT 01-JU

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                                                              Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                        MEDLINE=98165392; PubMed=9425133;
Appel B., Eisen J.S.;
"Regulation of neuronal specification in the zebrafish spinal cord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSI; ZDB-GENE-980526-29; dla.

GO; GO:0016020; C:membrane; IEA.
GO; GO:001504; P:calcium ion binding; IEA.
GO; GO:0001549; P:calcium ion binding; IEA.
GO; GO:0001549; P:calcium ion binding; IEA.
GO; GO:0001549; P:calcium ion binding; IEA.
InterPro; IPR001074; BSE.
InterPro; IPR00174; EGF_Ca.
InterPro; IPR00181; EGF_Ca.
InterPro; IPR00181; EGF_II.
InterPro; IPR00191; EGF_II.
InterPro; IPR001091; EGF_II.
PFam; PF001010; EGFELCOD.
SMART; SM00109; EGF_II.
SMART; SM00179; EGF_CA; 3.
PROSITE; PS001010; EGFELCOD.
SMART; SM00179; EGF_I; B.
PROSITE; PS01186; EGF_I; B.
PROSITE; PS01186; EGF_I; B.
PROSITE; PS01186; EGF_Z; B.
PROSITE; PS01187; EGF_Z; B.
PROSITE; PS01187; EGF_Z; B.
PROSITE; PS01187; EGF_Z; B.
PROSITE; PS01187; EGF_Z; B.
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EMBL; AF030031; AAC41249.1; -.
HSSP; P00740; 1EDM.
06,
26,
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Matches 442; Conservative
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A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blar N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heibh F.,
Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brown E.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mitching M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
N. Arzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                          Jonés S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                              -SPVSRCEH-PCHNGATCHRR----YCEC-AGYGG-NCQFLLPEPPGPVDEEQFPW-AVC
                                                             -CVDLGNSYCCQAGFG----RCDNV-DDCAS-PC-NGGTCDVNDS---CTCPPGY-GKNC
                      RCVDLVNSYLCQCPDGFTGMNCDRAGDECSMYPCQNGGTCQEGASGYMCTCPPGYTGRNC
                                                                                            AGLVLLLL---GCA-AVVCVRLK------QKPECETETMNNLA-NCQREKD---SS
                                                                                                                   SGVLLVLLVLLVVACAVVVVCVRSKVQORRRDREDEVANGENETINNLTNNCHRDKDLAVSV
                                                                                                                                           IGATQIKNTNKK-DF---HDK------KVRY-PVDYNLV------
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                       MGC52561 protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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                                                                                                                                                                                                                                          565 VYVSEK-DECIA 575
                                                                                                                                                                                                                                                                 757 KYSESKYSRCIA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVDDCA-SPC-NGGTC--DVND-SCTCPPGY-GKNCS-PVSRC-EHPCHNGATCHRRY-- 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --CEC-AGY-GGNCQFLLPEPPGPV----DEEQFPWAVCAGLV-LLLLGCAAVVCVR-- 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRGHFNEKGRVNNDLEPKNNLIEKEPHFKMPNPDYLREKSSSKQKLLQGSESEEERSGRR 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HDKK------VRYPVDYNLVLKVHKKCSEEKALRKRPSVYSTSKDTKYQSVYV-SEK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ISRL-TQRHL-VGEEWSQDLHSSGRTDL-YSYRFVCDEHYYGEGCSVFCRPRDD-FGHFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 KSSGVGYVCRCPFNYHGSNCEKKIDRCTNSPCLNGGQCLDMGRNVLCKCRPGFSGPRCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 SALLCV----SGVFELKLQEFVNKKGLLNRNCCRGGGCCTFFRVCLKHYQASVSPEPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AATLCLPLVYPAGVFELKIHSFSTPRPA----CAAGKSCNIFFRVCLKHAQPVVSPDPPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C---GRGEKCPGWKGQYCT-PICLPGC-DQHG-CDKPGECKCRVGWQGRYCDECIRYPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDEQGNRLCMSGWKGEYCAEPICLPGCSESHGFCELPGECKCRMGWOGELCDECLRYPGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDGG---YC-CPLG-SGFNCEKK--DC-SSPC--NGACVDLG-NSYC-CQAGFG--RCD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKPC-NGATCTNTGQGSYTCSCRPGYTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----IKQKPECETETMNNLANCQ------REKDSS----IGATQIKNTNKKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1383; DB 2; Length 6; Pred. No. 6.4e-93; 74; Mismatches 151; Indels
                                the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         642 AA; 70655 MW; 56AFB4013E1C2AE2 CRC64;
Klein S., Strausberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ
EMBL; BC044262; AAH44262.1; -.
HSSP; P00740; LEDM.
GO; GO:0016020; C:membrane; IEA.
GO; GO:001509; F:calcium ion binding; IEA.
GO; GO:00154; P:cell communication; IEA.
InterPro; IPR001154; P:cell communication; IEA.
InterPro; IPR001174; EGF_Z.
InterPro; IPR001174; EGF_Z.
InterPro; IPR001181; EGF_Z.
InterPro; IPR001181; EGF_Z.
InterPro; IPR001181; EGF_Z.
InterPro; IPR001181; EGF_II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.9%; Score 1383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00179; EGF CA; 3.

PROSITE; PS00010; ASX HYDROXYL; 2.

PROSITE; PS010021; EGF 2; 7.

PROSITE; PS01186; EGF 2; 7.

PROSITE; PS01187; EGF 2; 7.
                                                                                                                                                                                                                                                                                                                                    Pfam; PF01414; DSL; 1.
Pfam; PF00008; EGF; 5.
Pfam; PF07645; EGF CA; 1.
PRINTS; PR0010; EGFBLCOD.
SMART; SM00051; DSL; 1.
SMART; SM00179; EGF_CA; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 46.3%
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-like domain.
SEQUENCE 642 A
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Search completed: November 29, 2004, 13:26:08 Job time: 72.5872 secs